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OM nucleic - nucleic search, using sw model

Run on: August 12, 2004, 03:27:51 ; Search time 349 Seconds
(without alignments)
12708.216 Million cell updates/sec

Title: US-10-005-469-4

Perfect score: 7992

Sequence: 1 gccagcccccattggggc.....ctctdgcagatcaagtact 7992

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:*

- 1: /cgn2_6/prodata/2/ina/5A_COMB.seq:*
- 2: /cgn2_6/prodata/2/ina/5B_COMB.seq:*
- 3: /cgn2_6/prodata/2/ina/6A_COMB.seq:*
- 4: /cgn2_6/prodata/2/ina/6B_COMB.seq:*
- 5: /cgn2_6/prodata/2/ina/PTUS_COMB.seq:*
- 6: /cgn2_6/prodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7982.6	99.9	7989	4	US-09-539-601-10
2	7960.6	99.6	8001	4	US-09-539-601-7
3	7943	99.4	8001	4	US-09-539-601-22
4	7941.4	99.4	8001	4	US-09-539-601-16
5	7935	99.3	8001	4	US-09-539-601-28
6	7324.6	91.6	8637	4	US-09-539-601-4
7	7302.6	91.4	8649	4	US-09-539-601-13
8	6180.4	77.3	11076	4	US-09-539-601-1
9	6162.8	77.1	11076	4	US-09-539-601-25
10	6161.2	77.1	11076	4	US-09-539-601-19
11	6154.8	77.0	11076	4	US-09-539-601-31
12	5312	66.5	9595	3	US-09-014-416-4
13	5218	65.3	7917	1	US-08-324-977-31
14	5218	65.3	7917	2	US-08-384-616-31
15	5218	65.3	7917	2	US-08-304-686A-31
16	5218	65.3	7917	1	US-09-315-850-31
17	5218	65.3	9416	1	US-08-324-977-1
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19	5218	65.3	9416	3	US-08-904-686A-1
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22	5205.4	65.1	9472	4	US-08-150-204E-96
23	5175.2	64.8	7863	1	US-08-324-977-35
24	5175.2	64.8	7863	2	US-08-384-616-35
25	5175.2	64.8	7863	2	US-08-904-686A-35
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27	5175.2	64.8	9030	1	US-08-324-977-13

28 5175.2 64.8 9030 2 US-08-384-616-13 Sequence 13, Appl
29 5175.2 64.8 9030 2 US-08-904-686A-13 Sequence 13, Appl
30 5175.2 64.8 9030 3 US-09-315-850-13 Sequence 13, Appl
31 4100.6 51.3 9599 3 US-09-014-416-2 Sequence 2, Appl
32 4099 51.3 9599 3 US-09-014-416-6 Sequence 6, Appl
33 4094.6 51.2 9646 3 US-08-811-566-1 Sequence 1, Appl
34 4094.6 51.2 9646 4 US-09-034-756-1 Sequence 1, Appl
35 4091 51.2 12980 3 US-08-811-566-5 Sequence 5, Appl
36 4091 51.2 12980 4 US-09-034-756-5 Sequence 5, Appl
37 4018.2 50.3 9379 3 US-08-388-874-1 Sequence 1, Appl
38 4018.2 50.3 9379 4 US-09-916-359-1 Sequence 1, Appl
39 4018.2 50.3 9401 1 US-07-910-760-9 Sequence 9, Appl
40 4018.2 50.3 9401 1 US-08-440-519-9 Sequence 9, Appl
41 4018.2 50.3 9401 4 US-08-440-549-9 Sequence 9, Appl
42 4018.2 50.3 9401 4 US-08-823-895A-25 Sequence 25, Appl
43 4017.4 50.3 9401 5 PCT-US91-02225-9 Sequence 9, Appl
44 4016.2 50.3 9379 3 US-08-444-818-176 Sequence 176, App
45 3967.2 49.6 9416 3 US-08-811-566-19 Sequence 19, Appl

ALIGNMENTS

RESULT 1

US-09-539-601-10

Sequence 10, Application US/09539601C

Patent No. 6630343

GENERAL INFORMATION:

APPLICANT: Bartenschlager, Ralf FW

TITLE OF INVENTION: Hepatitis C Virus Cell Culture System

FILE REFERENCE: all sequences

CURRENT APPLICATION NUMBER: US/09/539,601C

CURRENT FILING DATE: 2001-08-30

EARLIER APPLICATION NUMBER: 199 15 178.4 GERMANY

EARLIER FILING DATE: 1999-04-03

NUMBER OF SEQ ID NOS: 51

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 10

LENGTH: 7989

TYPE: DNA

ORGANISM: Hepatitis C virus

FEATURE:

NAME/KEY: 5'UTR

LOCATION: (1)..(341)

OTHER INFORMATION: construct I377/NS3-3'/wt

FEATURE:

NAME/KEY: CDS

LOCATION: (342)..(1181)

OTHER INFORMATION: hepatitis C virus core-neomycin phosphotransferase

OTHER INFORMATION: fusion protein

FEATURE:

NAME/KEY: RBS

LOCATION: (1190)..(1800)

OTHER INFORMATION: internal ribosome entry site from

OTHER INFORMATION: encephalomyocarditis virus

FEATURE:

NAME/KEY: CDS

LOCATION: (1801)..(7758)

OTHER INFORMATION: hepatitis C virus NS3 - 5B

FEATURE:

NAME/KEY: 3'UTR

LOCATION: (7759)..(7989)

PUBLICATION INFORMATION:

AUTHORS: Lohmann, Volker

AUTHORS: Krner, Frank

AUTHORS: Koch, Jan-Oliver

AUTHORS: Herian, Ulrike

AUTHORS: Theilmann, Lorenz

AUTHORS: Bartenschlager, Ralf

TITLE: Replication of subgenomic hepatitis c virus RNAs in a

cell line

JOURNAL: Science

VOLUME: 285

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i;
US-09-539-601-10

PAGES: 110-113

DATE: 1999-07-02

Matches 7985; Conservative

Query Match 99.9%; Score 7982.6; DB 4; Length 7989;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 7985; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db 3421 ACCCACATAGACGCCCATTTCTGTCGAGCTAAGCAGCAGGAGACAACTTCCCTAC 3480
QY 3481 CTGTTAGCATACGAGGCTACGGTGTGCGCAGGGCTCAGGCTCCACCTCCATCTGTTGGAC 3540
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QY 3541 CAATGTGGAAGTGTCTCATACGCTAAAGCTTAAGCTGACGCGGCAACGCGCTGCTG 3600
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QY 4141 ACCCTCTGTTTAAACATCTGGGGGATGGTGGCGCGCCCACTTCTCTCCCGGCT 4200
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QY 7081 TCTTCAATTTGTCTAGTCGCGCAGTATGTCATGCGCAAGGCTGACTATCTCACCCGT 7140
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RESULT 2

US-09-539-601-7
; Sequence 7, Application US/09539601C
; Patent No. 6638343
; GENERAL INFORMATION:
; APPLICANT: Bartenschlager, Ralf FW
; TITLE OF INVENTION: Hepatitis C Virus Cell Culture System
; FILE REFERENCE: all sequences
; CURRENT APPLICATION NUMBER: US/09/539,601C
; CURRENT FILING DATE: 2001-08-30
; EARLIER APPLICATION NUMBER: 199 15 178.4 GERMANY
; EARLIER FILING DATE: 1999-04-03
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
; LENGTH: 8001
; TYPE: DNA
; ORGANISM: Hepatitis C virus
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)..(341)
; OTHER INFORMATION: construct I389/NS3-3'/wt
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (342)..(1193)
; OTHER INFORMATION: hepatitis C virus core-neomycin
; OTHER INFORMATION: phosphotransferase fusion protein
; FEATURE:
; NAME/KEY: RBS
; LOCATION: (1202)..(1812)
; OTHER INFORMATION: internal ribosome entry site from
; OTHER INFORMATION: encephalomyocarditis virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1813)..(7770)
; OTHER INFORMATION: hepatitis C virus nonstructural proteins NS3-5B
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: (7771)..(8001)

PUBLICATION INFORMATION:

AUTHORS: Lohmann, Volker
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 AUTHORS: Theilmann, Lorenz
 AUTHORS: Bartenschlager, Ralf
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 TITLE: hepatoma cell line
 JOURNAL: Science
 VOLUME: 285
 PAGES: 110-113
 DATE: 1999-07-02
 US-09-539-601-7

Query Match 99.6%; Score 7960.6; DB 4; Length 8001;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 7985; Conservative 0; Mismatches 4; Indels 12; Gaps 1;

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RESULT 3
US-09-539-601-22
; Sequence 22, Application US/09539601C
; Patent No. 6630343
; GENERAL INFORMATION:
; APPLICANT: Bartschschlager, Ralf FW
; TITLE OF INVENTION: Hepatitis C Virus Cell Culture System
; FILE REFERENCE: all sequences
; CURRENT APPLICATION NUMBER: US/09/539,601C
; CURRENT FILING DATE: 2001-08-30
; EARLIER APPLICATION NUMBER: 199 15 178.4 GERMANY
; EARLIER FILING DATE: 1999-04-03
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 8001
; TYPE: DNA
; ORGANISM: Hepatitis C virus
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)..(341)
; OTHER INFORMATION: construct I389/NS3-3'/5.1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (342)..(1193)
; OTHER INFORMATION: hepatitis C virus core - neomycin
; OTHER INFORMATION: phosphotransferase fusion protein
; FEATURE:

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; NAME/KEY: RBS
; LOCATION: (1202)..(1812)
; OTHER INFORMATION: internal ribosome entry site from
; OTHER INFORMATION: encephalomyocarditis virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1813)..(7770)
; OTHER INFORMATION: hepatitis C virus nonstructural proteins NS3 - 5B
; OTHER INFORMATION: of cell culture-adapted clone no. 5.1
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (7771)..(8001)
; US-09-539-601-22

Query Match      99.4%; Score 7943; DB 4; Length 8001;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 7974; Conservative 0; Mismatches 15; Indels 12; Gaps 1;

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Db	4141	ACCACCCAAACATACCTCTCTGTTTAAACATCTCTGGGGGATGGGTGGCGGCCAACTTGCT	4200	Qy	5269	ACGCGGAGACGCGTAAAGCGTAGGTCGCCAGGGATCTCCCTCTCTTTGGCCAGGTCA	5328
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Db	4321	CGCGTCTGGGCTTTAAGGTCAATGAGCGGCGAGATGCCCTCCACCGAGGACCTGGTTAAC	4380	Qy	5449	ACCCGCTGGAGTCAGAAATAGGTAGTAATTTGGACTCTTTTCGAGCGCTCCAGCG	5508
Qy	4369	CTACTCCCTGATCTCTCCCTGGGCGCTAGTCTGGGGTCTGTGGCAGCGATA	4428	Db	5461	ACCCGCTGGAGTCAGAAATAGGTAGTAATTTGGACTCTTTTCGAGCGCTCCAGCG	5520
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Qy	4549	GCAGTGTCACTCAGATCCTCTCTAGTCTTACCATCACTCAGCTGCTGAAGAGGTTTCA	4608	Db	5641	AAGGACCCGAGTACGTCCTCCAGTGTGACACGGGTCTCCATTCGCGCTGCCAAGGCC	5700
Db	4561	GCAGTGTCACTCAGATCCTCTCTAGTCTTACCATCACTCAGCTGCTGAAGAGGTTTCA	4620	Qy	5689	CCTCGATACCACTCTCCACGGAGGAGGACGGTGTCTCTGTCAAGATCTACCGTGTCT	5748
Qy	4609	CAGTGTCACTCAGATCCTCTCTAGTCTTACCATCACTCAGCTGCTGAAGAGGTTTGG	4668	Db	5701	CCTCGATACCACTCTCCACGGAGGAGGACGGTGTCTCTGTCAAGATCTACCGTGTCT	5760
Db	4621	CAGTGTCACTCAGATCCTCTCTAGTCTTACCATCACTCAGCTGCTGAAGAGGTTTGG	4680	Qy	5749	TTCTGCTTTGGCGAGCTCGCCAAAGACCTTTGGGAGCTTCGAATCTGTCGCGCGTGCAC	5808
Qy	4669	GATTGGATATGACCGGTGTGATGATTTCAAGCTCTGGCTCGAGTCCAGCTCTCGCG	4728	Db	5761	TTCTGCTTTGGCGAGCTCGCCAAAGACCTTTGGGAGCTTCGAATCTGTCGCGCGTGCAC	5820
Db	4681	GATTGGATATGACCGGTGTGATGATTTCAAGCTCTGGCTCGAGTCCAGCTCTCGCG	4740	Qy	5809	ACGCGCACGGCAACGGCTCTCTCGACAGCCCTCCGACGCGGCGACCGGATCCGAC	5868
Qy	4729	CGATTCCGGGAGTCCCTCTCTCATGTCAACGTGGGTACAAAGGAGTCTGGCGGGGC	4788	Db	5821	ACGCGCACGGCAACGGCTCTCTCGACAGCCCTCCGACGCGGCGACCGGATCCGAC	5880
Db	4741	CGATTCCGGGAGTCCCTCTCTCATGTCAACGTGGGTACAAAGGAGTCTGGCGGGC	4800	Qy	5869	GTGTAGTCTGATCTCTCTCATGCCCCCTTTGAGGGGAGCGCGGGGATCCGATCTCAGC	5928
Qy	4789	GACGGCATCATGCAAAACCACTGCCCATGTGGAGCAACATGCGGACATGCGGATGAAAAA	4848	Db	5881	GTGTAGTCTGATCTCTCTCATGCCCCCTTTGAGGGGAGCGCGGGGATCCGATCTCAGC	5940
Db	4801	GACGGCATCATGCAAAACCACTGCCCATGTGGAGCAACATGCGGACATGCGGATGAAAAA	4860	Qy	5929	GACGGCTTTGTTCTACCGTAAGCGAGGAGGCTAGTGAGGACGTCTGCTGCTCGATG	5988
Qy	4849	GGTTCCATGAGGATCGTGGGCTTAGGACCTGTAGTAAACAGTGGCATGGAATTCCTCC	4908	Db	5941	GACGGCTTTGTTCTACCGTAAGCGAGGAGGCTAGTGAGGACGTCTGCTGCTCGATG	6000
Db	4861	GGTTCCATGAGGATCGTGGGCTTAGGACCTGTAGTAAACAGTGGCATGGAATTCCTCC	4920	Qy	5989	TTCTACATGACAGCAGCGCCCTGATCAGCCATGCGCTGCGGAGGAAACCAAGCTGCC	6048
Qy	4909	ATTAAAGCGGTACACACGGGCGCTGACGCTCCCGGCGCAAAATTTCTAGGGCG	4968	Db	6001	TTCTACATGACAGCAGCGCCCTGATCAGCCATGCGCTGCGGAGGAAACCAAGCTGCC	6060
Db	4921	ATTAAAGCGGTACACACGGGCGCTGACGCTCCCGGCGCAAAATTTCTAGGGCG	4980	Qy	6049	ATCAATGCACTGAGCAACTCTTTGCTCCGTCAACCAACTTGTGTATGCTACAACTCT	6108
Qy	4969	CTGTGGCGGTGCTGCTGAGGAGTACGTGGAGTTACCGGGTGGGGGATTTCCATAC	5028	Db	6061	ATCAATGCACTGAGCAACTCTTTGCTCCGTCAACCAACTTGTGTATGCTACAACTCT	6120
Db	4981	CTGTGGCGGTGCTGCTGAGGAGTACGTGGAGTTACCGGGTGGGGGATTTCCATAC	5040	Qy	6109	CGAGCGCAAGCTCGCGGCAAGAGGTCACCTTTGACAGACTGCGAGTCTCTGGACGAC	6168
Qy	5029	GTAGCGGCAATGACCACTGACAGTAAAGTCCCGTGCAGTCTCCGGCCCGCAATTC	5088	Db	6121	CGAGCGCAAGCTCGCGGCAAGAGGTCACCTTTGACAGACTGCGAGTCTCTGGACGAC	6180
Db	5041	GTAGCGGCAATGACCACTGACAGTAAAGTCCCGTGCAGTCTCCGGCCCGCAATTC	5100	Qy	6169	CATCTACCGGAGCTGTCTCAAGGAGATGAAGCGGAGGCGTCCACAGTTAAGGCTTAACT	6228
Qy	5089	TTACAGAAATGATGGGTGCGGTGTGACAGAGTACGCTCCAGCGTGCAAAACCCCTCCTA	5148	Db	6181	CATCTACCGGAGCTGTCTCAAGGAGATGAAGCGGAGGCGTCCACAGTTAAGGCTTAACT	6240
Db	5101	TTACAGAAATGATGGGTGCGGTGTGACAGAGTACGCTCCAGCGTGCAAAACCCCTCCTA	5160	Qy	6229	CTATCCGTGGAGGAGCTGTAAAGTGAACCGCCCACTTCGCGGACATCTAAATTTGGC	6288
Qy	5149	CGGAGGAGGTCAATTCCTGGTGGGCTCAATACATACCTGTTGGTCAAGCTCCCA	5208	Db	6241	CTATCCGTGGAGGAGCTGTAAAGTGAACCGCCCACTTCGCGGACATCTAAATTTGGC	6300
Db	5161	CGGAGGAGGTCAATTCCTGGTGGGCTCAATACATACCTGTTGGTCAAGCTCCCA	5220				

QY 6289 TATGGGGCAAGAGCGTCCGGAACCTATCCAGCAGGCGGTTAAACCAATCCGCTCCGCTG 6348
Db 6301 TATGGGGCAAGAGCGTCCGGAACCTATCCAGCAGGCGGTTAAACCAATCCGCTCCGCTG 6360
QY 6349 TGGAGGACTTGGTGGAGACACTGAGACACCAATTTGACACCAATCATGCGCAAAAAT 6408
Db 6361 TGGAGGACTTGGTGGAGACACTGAGACACCAATTTGACACCAATCATGCGCAAAAAT 6420
QY 6409 GAGGTTTTCGCTCCAAACAGAGAAAGGGGGCGCGCAAGCGCTCCGCTTATCGTATTC 6468
Db 6421 GAGGTTTTCGCTCCAAACAGAGAAAGGGGGCGCGCAAGCGCTCCGCTTATCGTATTC 6480
QY 6469 CCAGATTGGGGGTCGTGTGTGCGAGAAATGGCCCTTTACGATGTGGTCTCCACCCCTC 6528
Db 6481 CCAGATTGGGGGTCGTGTGTGCGAGAAATGGCCCTTTACGATGTGGTCTCCACCCCTC 6540
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QY 6589 TTCTGTGTAATGCTTGGAAAGCGAAGAAATGCCCTATGGCTTCGCAATATGACACCCGC 6648
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QY 6649 TGTGTTGACTCAACGGTCACTGAGAAATGACATCCGTTTGAGGAGTCAATCTACCAATGT 6708
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QY 6769 GGGGGCCCCCTGACTAATCTAAAGGCGAAGCTGCGGCTATCGCGGTGCGCGCGGAGC 6828
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QY 6829 GGTGTACTGACGACAGCTGCGGTAAATACCTCACAATGTTACTTGAAGCGCGCTGCGGCG 6888
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QY 6889 TGTGAGCTGCGAGCTCCAGGACTGACGATGCTGATGCGGAGACGACCTTGTGCTT 6948
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QY 6949 ATCTGTAAAGCGCGGGGACCAAGAGGACGAGGAGCTACGCGCTTACGAGGCT 7008
Db 6961 ATCTGTAAAGCGCGGGACCAAGAGGACGAGGAGCTACGCGCTTACGAGGCT 7020
QY 7009 ATGACTAGATCTCTGCCCCCTCTGGGACCGCCCAACCCAGAAATACGACTTGGAGTTG 7068
Db 7021 ATGACTAGATCTCTGCCCCCTCTGGGACCGCCCAACCCAGAAATACGACTTGGAGTTG 7080
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QY 7129 TATCTACCCGTGACCCCAACCCCTTGTGCGGCGCTGCGTGGGAGACAGCTAGACAC 7188
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QY 7189 ACTCAGTCAATCTCTGGGTAGGCAACATCATGATATGCGCCCACTTGTGGGCAAGG 7248
Db 7201 ACTCAGTCAATCTCTGGGTAGGCAACATCATGATATGCGCCCACTTGTGGGCAAGG 7260
QY 7249 ATGATCTGATGACTCAATCTCTCCATCTTCTAGCTCAGGAACAACTTGA AAAAGCC 7308
Db 7261 ATGATCTGATGACTCAATCTCTCCATCTTCTAGCTCAGGAACAACTTGA AAAAGCC 7320
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Db 7321 CTAGATTCTCAGATCTAGCGGCGCTTGTACTCCATTGAGGCACTTGACTACCTCAGATC 7380
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Db 7381 ATTCACGACTCCATGGCCTTAGCGCAATTTTCACTCCATAGTTACTCTCCAGGTGAGATC 7440
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QY 7489 CGGCGCAGAAAGTGTCCGCGTCTAGGCTACTGTCCAGGGGGGAGGGCTGCCACTTGTGGC 7548
Db 7501 CGGCGCAGAAAGTGTCCGCGTCTAGGCTACTGTCCAGGGGGGAGGGCTGCCACTTGTGGC 7560
QY 7549 AAGTACCTCTTCAACTGGGAGTAAGACCAAGCTCAAACTCAACTCCAAATCCCGGCTGCG 7608
Db 7561 AAGTACCTCTTCAACTGGGAGTAAGACCAAGCTCAAACTCAACTCCAAATCCCGGCTGCG 7620
QY 7609 TCCAGTTGGAATTTATCCAGCTGTTTGGTGTGTTTACAGCGGGGAGACATATATCAC 7668
Db 7621 TCCAGTTGGAATTTATCCAGCTGTTTGGTGTGTTTACAGCGGGGAGACATATATCAC 7680
QY 7669 AGCTGTCTGTCGCGCGACCCCGCTGTTTCATGTGTGCTTCTCTTCTGTAGGG 7728
Db 7681 AGCTGTCTGTCGCGCGACCCCGCTGTTTCATGTGTGCTTCTCTTCTGTAGGG 7740
QY 7729 GTAGGCACTATCTACTCTCCCAACCGATGAAACCGGAGCTAAACACTCCAGGCAATAGG 7788
Db 7741 GTAGGCACTATCTACTCTCCCAACCGATGAAACCGGAGCTAAACACTCCAGGCAATAGG 7800
QY 7789 CCATCTGTTTTTTTCCCTTT 7848
Db 7801 CCATCTGTTTTTTTCCCTTT 7860
QY 7849 TTTTCTCTTTTTTTTTTCTTTTTTCTTTTTTCTTTTTTCTTTTGTGGTGGCTTCACTTAGC 7908
Db 7861 TTTTCTCTTTTTTTTTTCTTTTTTCTTTTTTCTTTTTTCTTTTGTGGTGGCTTCACTTAGC 7920
QY 7909 CCTAGTCACGGCTAGCTGTGAAGGTCCTGAGCGCGCTTGAAGTCTGAGAGTCTGATC 7968
Db 7921 CCTAGTCACGGCTAGCTGTGAAGGTCCTGAGCGCGCTTGAAGTCTGAGAGTCTGATC 7980
QY 7969 TGGCCTCTCTGCAGATCAAGT 7989
Db 7981 TGGCCTCTCTGCAGATCAAGT 8001

RESULT 4
US-09-539-601-16
; Sequence 16, Application US/09539601C
; Patent No. 6630343
; GENERAL INFORMATION:
; APPLICANT: Bartenschlager, Ralf FW
; TITLE OF INVENTION: Hepatitis C Virus Cell Culture System
; FILE REFERENCE: all sequences
; CURRENT APPLICATION NUMBER: US/09/539,601C
; CURRENT FILING DATE: 2001-08-30
; EARLIER APPLICATION NUMBER: 199 15 178.4 GERMANY
; EARLIER FILING DATE: 1999-04-03
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 16
; LENGTH: 8001
; TYPE: DNA
; ORGANISM: Hepatitis C virus
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)..(341)
; OTHER INFORMATION: construct 1389/NS3-3'/9-13F
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (342)..(1193)
; OTHER INFORMATION: hepatitis C virus core-neomycin phosphotransferase
; OTHER INFORMATION: fusion protein
; FEATURE:
; NAME/KEY: RBS

Mon Aug 16 09:32:31 2004

LOCATION: (1202)..(1812)
OTHER INFORMATION: internal ribosome entry site from
OTHER INFORMATION: encephalomyocarditis virus
FEATURE:
NAME/KEY: CDS
LOCATION: (1813)..(7770)
OTHER INFORMATION: hepatitis C virus nonstructural protein NS3-5B;
OTHER INFORMATION: carries cell culture-adaptive mutations from clone
OTHER INFORMATION: 9-13F
FEATURE:
NAME/KEY: 3'UTR
LOCATION: (7771)..(8001)
US-09-539-601-16

Query Match 99.4%; Score 7941.4; DB 4; Length 8001;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 7973; Conservative 0; Mismatches 16; Indels 12; Gaps 1;

Qy	1	GCCAGCCCCGATTTGGGGGACACTCCACCATAGATCACTCCCTGTGAGGAATCTAG	60
Db	1	GCCAGCCCCGATTTGGGGGACACTCCACCATAGATCACTCCCTGTGAGGAATCTAG	60
Qy	61	TCATTACGCGAAGAGCTAGCCATGCGTTAGTATGAGTGTGCTGAGGCTCCAGGAC	120
Db	61	TCATTACGCGAAGAGCTAGCCATGCGTTAGTATGAGTGTGCTGAGGCTCCAGGAC	120
Qy	121	CCCCCTCCCGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACACCGGAATGGCCAG	180
Db	121	CCCCCTCCCGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACACCGGAATGGCCAG	180
Qy	181	GACGACCGGGTCTTTCTTGGATCAACCCGCTCAATGCTGAGAGTTGGGGTGGCCCC	240
Db	181	GACGACCGGGTCTTTCTTGGATCAACCCGCTCAATGCTGAGAGTTGGGGTGGCCCC	240
Qy	241	GCGAGACTGTAGCGAGTGTGGTTCGGAAGGCTTGTGCTACTGCTGATAGG	300
Db	241	GCGAGACTGTAGCGAGTGTGGTTCGGAAGGCTTGTGCTACTGCTGATAGG	300
Qy	301	GTGCTTGGAGTGTCCCGGGAGGCTCTCGTAGCCGTGACCAATGAGCAGCAATCTTAAC	360
Db	301	GTGCTTGGAGTGTCCCGGGAGGCTCTCGTAGCCGTGACCAATGAGCAGCAATCTTAAC	360
Qy	361	CTCAAGAAAAACCAA-----GGCGCGCCATGATGAACAGATGATGTC	408
Db	361	CTCAAGAAAAACCAA-----GGCGCGCCATGATGAACAGATGATGTC	420
Qy	409	ACGAGGTTCTCCGGCGCTTGGGTGGAGAGCTATTGGCTATGATGAGGCAACAGA	468
Db	421	ACGAGGTTCTCCGGCGCTTGGGTGGAGAGCTATTGGCTATGATGAGGCAACAGA	480
Qy	469	CAATCGGCTGTCTGATGCGCGCTGTTCCGGCTGTACGCGAGGGGCGCGGTTCTTT	528
Db	481	CAATCGGCTGTCTGATGCGCGCTGTTCCGGCTGTACGCGAGGGGCGCGGTTCTTT	540
Qy	529	TTGTCAAGCAACCTGCTCGGCTGAATGAATGAGCTGAGCAGGAGGCGCGCTAT	588
Db	541	TTGTCAAGCAACCTGCTCGGCTGAATGAATGAGCTGAGCAGGAGGCGCGCTAT	600
Qy	589	CGTGGTGGCCACGAGCGGCTTCTTGGCGAGCTGTGCTGCAAGTGTCACTGAAGCGG	648
Db	601	CGTGGTGGCCACGAGCGGCTTCTTGGCGAGTGTGCTGCAAGTGTCACTGAAGCGG	660
Qy	649	GAGGAGCTGGTGTCTATTGGGCGAAGTGCCGGGGCAGGATCTCCTGTATCTCACTTG	708
Db	661	GAGGAGCTGGTGTCTATTGGGCGAAGTGCCGGGGCAGGATCTCCTGTATCTCACTTG	720
Qy	709	CTCCTCCGAGAAAGTATCCATCATGCTGATGCAATGGCGGCTGCATACCTTTGATC	768
Db	721	CTCCTCCGAGAAAGTATCCATCATGCTGATGCAATGGCGGCTGCATACCTTTGATC	780
Qy	769	CGGCTACCTGCCATTCGACCAACAAAGCAAAACATGCAATCGAGCGAGCAGTCTCGGA	828
Db	781	CGGCTACCTGCCATTCGACCAACAAAGCAAAACATGCAATCGAGCGAGCAGTCTCGGA	840

Qy	829	TGGAAGCCGGTCTTGTGATCAGGATGATCTGGACGAGAGCATCAGGGCTCGCGCCAG	888
Db	841	TGGAAGCCGGTCTTGTGATCAGGATGATCTGGACGAGAGCATCAGGGCTCGCGCCAG	900
Qy	889	CCGAATGTTTGGCCAGGCTCAAGGCGCGCATGCGCGAGGAGATCTCGTGTGACCC	948
Db	901	CCGAATGTTTGGCCAGGCTCAAGGCGCGCATGCGCGAGGAGATCTCGTGTGACCC	960
Qy	949	ATGCGAATGCTGTTGCGCGAATATCATGATGGAATGCGCGCTTTCTGGATTATCG	1008
Db	961	ATGCGAATGCTGTTGCGCGAATATCATGATGGAATGCGCGCTTTCTGGATTATCG	1020
Qy	1009	ACTGTGCGCGGCTGGGTGTGCGGACCGCTATCAGGACATAGCTTGGCTACCGTGATA	1068
Db	1021	ACTGTGCGCGGCTGGGTGTGCGGACCGCTATCAGGACATAGCTTGGCTACCGTGATA	1080
Qy	1069	TTGCTGAAGAGCTTTGGCGCGAATGGGCTGACCGCTTCTCGTGTGCTTACGGTATCGCG	1128
Db	1081	TTGCTGAAGAGCTTTGGCGCGAATGGGCTGACCGCTTCTCGTGTGCTTACGGTATCGCG	1140
Qy	1129	CTCCCGATTGCGAGCGCATGCGCTTCTATCGCTTCTTGACGAGTCTTCTGAGTTAAA	1188
Db	1141	CTCCCGATTGCGAGCGCATGCGCTTCTATCGCTTCTTGACGAGTCTTCTGAGTTAAA	1200
Qy	1189	CAGACCAACACGCTTCCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCT	1248
Db	1201	CAGACCAACACGCTTCCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCT	1260
Qy	1249	AACGTTACTGCGCAAGCGCTTGAATAAGCGCGGTGCTGCTTGTGCTATATGTTAT	1308
Db	1261	AACGTTACTGCGCAAGCGCTTGAATAAGCGCGGTGCTGCTTGTGCTATATGTTAT	1320
Qy	1309	TCCACCATTTGCGCTCTTTTGGCAATGTGAGGCGCGGAAACCTGCGCCCTCTCTTTG	1368
Db	1321	TCCACCATTTGCGCTCTTTTGGCAATGTGAGGCGCGGAAACCTGCGCCCTCTCTTTG	1380
Qy	1369	ACGAGCATTCCTAGGGGTCTTTTCCCTCTCGCCAAAGGAATGCAAGGCTCTGTTGAATGTC	1428
Db	1381	ACGAGCATTCCTAGGGGTCTTTTCCCTCTCGCCAAAGGAATGCAAGGCTCTGTTGAATGTC	1440
Qy	1429	GTGAAGAGAGAGTTCCTCTGGAAGCTTCTTGAAGACAAACACCTGCTGAGCGACCTT	1488
Db	1441	GTGAAGAGAGAGTTCCTCTGGAAGCTTCTTGAAGACAAACACCTGCTGAGCGACCTT	1500
Qy	1489	TCCAGGAGCGGAACCCCGCCCTCGGCGACAGCTCTCGCGCAAAAGCAAGCTGTA	1548
Db	1501	TCCAGGAGCGGAACCCCGCCCTCGGCGACAGCTCTCGCGCAAAAGCAAGCTGTA	1560
Qy	1549	TAAAGATACCTGCAAGGCGGCAACCCCGAGTGCACGTTGTGAGTTGAGTGTG	1608
Db	1561	TAAAGATACCTGCAAGGCGGCAACCCCGAGTGCACGTTGTGAGTTGAGTGTG	1620
Qy	1609	GAAAGAGTCAAAATGGCTCTCCTAAGCGTATTCACAGGGGCTGAGGATGCCAGAG	1668
Db	1621	GAAAGAGTCAAAATGGCTCTCCTAAGCGTATTCACAGGGGCTGAGGATGCCAGAG	1680
Qy	1669	GTACCCCATTTGATGAGATCTCATCTGGGGCTCGGTGACATGCTTTACATGTTTAT	1728
Db	1681	GTACCCCATTTGATGAGATCTCATCTGGGGCTCGGTGACATGCTTTACATGTTTAT	1740
Qy	1729	TGAGGTTAAAAACGCTTAGGCCCCCGAAACAGGGGAGCGTGGTTTCTTTGAAAAA	1788
Db	1741	TGAGGTTAAAAACGCTTAGGCCCCCGAAACAGGGGAGCGTGGTTTCTTTGAAAAA	1800
Qy	1789	CAGGATAATACCATGCGGCTATTAGGCTCTCTCCCAACAGACGCGAGGCTTCTTGGC	1848
Db	1801	CAGGATAATACCATGCGGCTATTAGGCTCTCTCCCAACAGACGCGAGGCTTCTTGGC	1860
Qy	1849	TGCATCATCACTAGCTTCACAGCGCGGACAGGAACAGGTTCGAGGGGAGGTCCAGGT	1908
Db	1861	TGCATCATCACTAGCTTCACAGCGCGGACAGGAACAGGTTCGAGGGGAGGTCCAGGT	1920

QY	1909	GTCTCACCAGCAACAATCTTTCTCTGGCGACTTCGCTCAATGGCGTGTGTTGACTGTC	1968
Db	1921	GTCTCACCAGCAACAATCTTTCTCTGGCGACTTCGCTCAATGGCGTGTGTTGACTGTC	1980
QY	1969	TATCATGGTGC GGCTCAAGACCCCTTCGGGCCCAAGGGCCCAATCACCCTAATGTAC	2028
Db	1981	TATCATGGTGC GGCTCAAGACCCCTTCGGGCCCAAGGGCCCAATCACCCTAATGTAC	2040
QY	2029	ACCAATGTGGACACGAGCACTCGTTCGGCTGGCAAGCGCCCGGGGGCGGTCCTTGACA	2088
Db	2041	ACCAATGTGGACACGAGCACTCGTTCGGCTGGCAAGCGCCCGGGGGCGGTCCTTGACA	2100
QY	2089	CCATGCACCTGCGGAGCTCGGACCTTTACTTTGTTTCAGAGGCATGCCGATGCTCATTCGG	2148
Db	2101	CCATGCACCTGCGGAGCTCGGACCTTTACTTTGTTTCAGAGGCATGCCGATGCTCATTCGG	2160
QY	2149	GTGCGCCGGCGGGCGACAGCAGGGGAGCTACTCTCCGCCAGGCCGCTCTCTACTTG	2208
Db	2161	GTGCGCCGGCGGGCGACAGCAGGGGAGCTACTCTCCGCCAGGCCGCTCTCTACTTG	2220
QY	2209	AAGGCTCTTTCGGGCGGTCCACTGCTCTGCCCTCGGGGACGCTGTGGCAGCTCTTCGG	2268
Db	2221	AAGGCTCTTTCGGGCGGTCCACTGCTCTGCCCTCGGGGACGCTGTGGCAGCTCTTCGG	2280
QY	2269	GCTGCCGTGTGCACCCGAGGGGTTTCGAAAGCGGTGGACTTTGTACCCGTCGAGTCTATG	2328
Db	2281	GCTGCCGTGTGCACCCGAGGGGTTTCGAAAGCGGTGGACTTTGTACCCGTCGAGTCTATG	2340
QY	2329	GAAGACCACTATGCCGTCCCCTCTTTCACGGAGAACTCGTCCCTTCGGCCGTACCGAG	2388
Db	2341	GAAGACCACTATGCCGTCCCCTCTTTCACGGAGAACTCGTCCCTTCGGCCGTACCGAG	2400
QY	2389	ACATTCAGGTGGCCCATCTACACGCCCTTACTGTTAGCGGCAAGAGCACTAAGGTGCCG	2448
Db	2401	ACATTCAGGTGGCCCATCTACACGCCCTTACTGTTAGCGGCAAGAGCACTAAGGTGCCG	2460
QY	2449	GCTCGGTATGCAGCCCAAGGTTAAGGTGCTTGTCTGTGAACCCCTCGGTGCGCGCACG	2508
Db	2461	GCTCGGTATGCAGCCCAAGGTTAAGGTGCTTGTCTGTGAACCCCTCGGTGCGCGCACG	2520
QY	2509	CTAGGTTTCGGGGGTATATGCTTAAGGCACATGGTATCGACCTTAACATCAGAACCGGG	2568
Db	2521	CTAGGTTTCGGGGGTATATGCTTAAGGCACATGGTATCGACCTTAACATCAGAACCGGG	2580
QY	2569	GTAAGGACCATCACCGCGTGCCTCCCATCAGCTACTCCACCTATGSGCAGTTCTTGCC	2628
Db	2581	GTAAGGACCATCACCGCGTGCCTCCCATCAGCTACTCCACCTATGSGCAGTTCTTGCC	2640
QY	2629	GACGTTGGTTGCTCTGGGGCGCTATGACATCATTAATATGATGAGTGCACCTCAACT	2688
Db	2641	GACGTTGGTTGCTCTGGGGCGCTATGACATCATTAATATGATGAGTGCACCTCAACT	2700
QY	2689	GACTCGACCACTATCTGGGCATCGCACAGTCCCTGGACCAAGCGGACGCTGGAGGG	2748
Db	2701	GACTCGACCACTATCTGGGCATCGCACAGTCCCTGGACCAAGCGGACGCTGGAGGG	2760
QY	2749	CGACTCGTGTGCTGCCACCGCTACGCCCTCGGGATCGGTCAACGTCACATCCAAAC	2808
Db	2761	CGACTCGTGTGCTGCCACCGCTACGCCCTCGGGATCGGTCAACGTCACATCCAAAC	2820
QY	2809	ATCGAGAGGTGCTCTGTACGACTGGAGAAATCCCTTTTATGGCAAAGCCATCCCC	2868
Db	2821	ATCGAGAGGTGCTCTGTACGACTGGAGAAATCCCTTTTATGGCAAAGCCATCCCC	2880
QY	2869	ATCGAGACCATCAAGGGGGAGGCACCTCATTTTCTGCCATTCCAAGAGAAATGTGAT	2928
Db	2881	ATCGAGACCATCAAGGGGGAGGCACCTCATTTTCTGCCATTCCAAGAGAAATGTGAT	2940
QY	2929	GAGCTCCGCGAAGCTGTCCGGCTTCGGACTCAATGTGTAGCATATTTACGGGGCCTT	2988
Db	2941	GAGCTCCGCGAAGCTATCCGGCTTCGGACTCAATGTGTAGCATATTTACGGGGCCTT	3000
QY	2989	GATGTATCCGTATACCAACTAGCGAGAGCTCATTTGTGTAGCAACGAGCTCTAATG	3048

Db	4081	CTTGGCAACCCCGATAGCATCACTGATGGCAATTCACAGCTCTATCACCAGCCCGCTC	4140	QY	5209	TGCGAGCCCGAACCAGTAGCAGTGTCTCACTTCATGTCTACCGACCCCTCCCAATT	5268
QY	4129	ACCACCCAAATACCTCTCTGTTTAAATCCTGGGGGATGGGTGGCCGCCCAATTGCT	4188	Db	5221	TGCGGCCCGAACCAGAGCTAGCAGTGTCTCACTTCATGTCTACCGACCCCTCCCAATT	5280
Db	4141	ACCACCCAAATACCTCTCTGTTTAAATCCTGGGGGATGGGTGGCCGCCCAATTGCT	4200	QY	5269	ACGCGGAGACGGCTAAGCGTAGGCTGGCCAGGGAGTCTCCCGCTCTTTGGCCAGTCA	5328
QY	4189	CTTCCACGAGCTGCTCTCTGTTTGGTAGGCGCGGATATCGCTGGAGCGGCTTTGGCAGC	4248	Db	5281	ACGCGGAGACGGCTAAGCGTAGGCTGGCCAGGGAGTCTCCCGCTCTTTGGCCAGTCA	5340
Db	4201	CTTCCACGAGCTGCTCTCTGTTTGGTAGGCGCGGATATCGCTGGAGCGGCTTTGGCAGC	4260	QY	5329	TCAGCTAGCAGCTGTCTGCGCTTCTTTCAGGCAACATGCACTACCGCTCATGATCC	5388
QY	4249	ATAGGCTTGGGAAGTGTCTGATATTTGGCAGTTATGAGAGGAGGCTGGCAGGC	4308	Db	5341	TCAGCTAGCAGCTGTCTGCGCTTCTTTCAGGCAACATGCACTACCGCTCATGATCC	5400
Db	4261	ATAGGCTTGGGAAGTGTCTGATATTTGGCAGTTATGAGAGGAGGCTGGCAGGC	4320	QY	5389	CCGAGCCTCACTCATCGAGGCAACCTCTCTGCGGCGAGAGATGGCGGGAATC	5448
QY	4309	GCGCTGCTGGCTTTAAGTGCATGAGCGGCGAGATGCCCTCCACCGAGGACCTGGCTAAC	4368	Db	5401	CCGAGCCTCACTCATCGAGGCAACCTCTCTGCGGCGAGAGATGGCGGGAATC	5460
Db	4321	GCGCTGCTGGCTTTAAGTGCATGAGCGGCGAGATGCCCTCCACCGAGGACCTGGTTAAC	4380	QY	5449	ACCCGCTGGAGTCAGAAAATAAGGTAGTAATTTTGGACTCTTTCGAGCCGCTCCAGCG	5508
QY	4369	CTACTCCCTGTATCTCTCTCCCTGGGCCCTAGTCTGCGGGTCTGTGCGCAGCGATA	4428	Db	5461	ACCCGCTGGAGTCAGAAAATAAGGTAGTAATTTTGGACTCTTTCGAGCCGCTCCAGCG	5520
Db	4381	CTACTCCCTGTATCTCTCTCCCTGGGCCCTAGTCTGCGGGTCTGTGCGCAGCGATA	4440	QY	5509	GAGGAGATGAGAGGAGATATCCGTTCCGCGCGAGATCCCTGCGGAGGTCAGGAAATTC	5568
QY	4429	CTGCGTCGGCAGTGGCCAGGGGAGGGGCTGTGCAATGATGAACCCGCTGATAGCG	4488	Db	5521	GAGGAGATGAGAGGAGATATCCGTTCCGCGCGAGATCCCTGCGGAGGTCAGGAAATTC	5580
Db	4441	CTGCGTCGGCAGTGGCCAGGGGAGGGGCTGTGCAATGATGAACCCGCTGATAGCG	4500	QY	5569	CCTCGAGCGATGCGCATATGGGCAACGCGCGGATTAACAACCTTCCATCTTTAGAGTCTTGG	5628
QY	4489	TTGCGCTCGCGGGTAAACAGCTCTCCCGCCAGCACTATGTCCTTGAGAGGACGCTGCA	4548	Db	5581	CCTCGAGCGATGCGCATATGGGCAACGCGCGGATTAACAACCTTCCATCTTTAGAGTCTTGG	5640
Db	4501	TTGCGCTCGCGGGTAAACAGCTCTCCCGCCAGCACTATGTCCTTGAGAGGACGCTGCA	4560	QY	5629	AAGGACCCGAGTACGTCCTTCCAGTGTGATACAGCGGTGTCCATTTGCGCGCTGCCAAGGCC	5688
QY	4549	GCACGTGCTACCTAGATCCTCTTAGTCTTAGCATCTACCTAGCTCTGAGAGGCTTCCAC	4608	Db	5641	AAGGACCCGAGTACGTCCTTCCAGTGTGATACAGCGGTGTCCATTTGCGCGCTGCCAAGGCC	5700
Db	4561	GCACGTGCTACCTAGATCCTCTTAGTCTTAGCATCTACCTAGCTCTGAGAGGCTTCCAC	4620	QY	5689	CCTCGATACCACTCCACGAGGAGAGGAGCGTGTCTCTGTCAGAAATCTACCGTGTCT	5748
QY	4609	CAGTGGATCAAGAGGAGTCTCCAGCGCATCTCGGCTCGTGGCTAAGAGATTTGG	4668	Db	5701	CCTCGATACCACTCCACGAGGAGAGGAGCGTGTCTCTGTCAGAAATCTACCGTGTCT	5760
Db	4621	CAGTGGATCAAGAGGAGTCTCCAGCGCATCTCGGCTCGTGGCTAAGAGATTTGG	4680	QY	5749	CTGTCCTTTGGGAGCTCGCCAAAGACCTTTGCGAGCTCCGAATCTGTCGCGCTCGAC	5808
QY	4669	GATTGGATATGACGGTGTGACTGATTTCAAGACCTGGCTCCAGTCCAGTCTCTGCGG	4728	Db	5761	CTGTCCTTTGGGAGCTCGCCAAAGACCTTTGCGAGCTCCGAATCTGTCGCGCTCGAC	5820
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Db	4741	CGATTGCGGGAGTCCCTCTTCTCATGTCAACGTGGTCAAGAGGAGTCTGGCGGGC	4800	QY	5869	GTTGAGTCTGATCTCTCTCATGCCCCCTTTGAGGGGAGCGCGGGGATCCCGATCTCAGC	5928
QY	4789	GACGGATCATGCAAAACCTGCGCATGTGAGCACAGATCACCGGACATGTGAAAAA	4848	Db	5881	GTTGAGTCTGATCTCTCTCATGCCCCCTTTGAGGGGAGCGCGGGGATCCCGATCTCAGC	5940
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QY	4849	GGTTCCATGAGGATCGTGGGCTTAGGACCTGTAGTAAACAGTGGCATGGAACATTTCCC	4908	Db	5941	GACGGTCTTGGTCTACCGTAAGCGAGGAGGCTAGTGAGGAGCTGTCTGCTGCTCGATG	6000
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QY	4969	CTGTGGCGGTGCTCTGAGGAGTACGTGGAGTTACGCGGTGGGGATTTCCACTAC	5028	Db	6061	GTCAATGCACTGAGCAACTTTTGTCTCCGTTCACCAACCTTGTGTATGTCTATGCTA	6120
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QY	5029	GTACCGGCGATGACCACTGACAAAGTAAAGTGGCGGTGTCAGTTCCGGCCCGGATTC	5088	Db	6121	CGCAGCGCAAGCTGCGGAGGAGGATCACTTTGACAGACTGCGAGGCTCTCGGAGC	6180
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RESULT 5
US-09-539-601-28
; Sequence 28, Application US/09539601C
; Patent No. 6630343
; GENERAL INFORMATION:
; APPLICANT: Bartenschlager, Ralf FW
; TITLE OF INVENTION: Hepatitis C Virus Cell Culture System
; FILE REFERENCE: all sequences
; CURRENT APPLICATION NUMBER: US/09/539,601C
; CURRENT FILING DATE: 2001-08-30
; EARLIER APPLICATION NUMBER: 199 15 178.4 GERMANY
; EARLIER FILING DATE: 1999-04-03
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 8001
; TYPE: DNA
; ORGANISM: Hepatitis C virus
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)..(341)
; OTHER INFORMATION: construct I389/NS3-3'/19
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (342)..(1193)
; OTHER INFORMATION: hepatitis C virus core - neomycin
; OTHER INFORMATION: phosphotransferase fusion protein
; FEATURE:
; NAME/KEY: RBS

LOCATION: (1202)...(1812)
; OTHER INFORMATION: internal ribosome entry site from
; OTHER INFORMATION: encephalomyocarditis virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1813)...(7770)
; OTHER INFORMATION: hepatitis C virus nonstructural proteins NS3 - 5B
; OTHER INFORMATION: of cell culture adapted clone no. 19
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: (7771)...(8001)
US-09-539-601-28

Query Match 99.3%; Score 7935; DB 4; Length 8001;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 7969; Conservative 0; Mismatches 20; Indels 12; Gaps 1;

QY 1 GCCAGCCCCGATTGGGGGCGACACTCCACCATAGATCACTCCCTGTGAGGAATACTG 60
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QY 61 TCTTCAAGCAGAAAGCGCTTAGCCATGCGCTTAGTATGAGTGTGCTGAGGCTCCAGGAC 120
DB 61 TCTTCAAGCAGAAAGCGCTTAGCCATGCGCTTAGTATGAGTGTGCTGAGGCTCCAGGAC 120

QY 121 CCCCCCTCCGGGAGAGCCTAGTGGTCTGGGAACCGGTGAGTACACCGGAATTGCCAG 180
DB 121 CCCCCCTCCGGGAGAGCCTAGTGGTCTGGGAACCGGTGAGTACACCGGAATTGCCAG 180

QY 181 GACGACCGGTCTCTTCTTGATCAACCGCTCAATGCTCGAGATTGGGGTGGCCCCC 240
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QY 241 GCGAGCTGTAGCGAGTAGTGTGGTTCGGAAGCCCTTGTGCTACTGCTGATAGG 300
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QY 361 CTCAAGAAACCAAA-----GGCGCGCCATGATTGAACAAGATGATTGC 408
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QY TTTACAGGCTCAACCATAGAGCGCCCATTTCTTGTCCAGACTAAGCAGGAGGAGGAGC 3468
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7981 TGGCTCTCTGCGAGATCAAGT 8001

RESULT 6
US-09-539-601-4
; Sequence 4, Application US/09539601C
; Patent No. 6630343
; GENERAL INFORMATION:
; APPLICANT: Bartenschlager, Ralf FW
; TITLE OF INVENTION: Hepatitis C Virus Cell Culture System
; FILE REFERENCE: all sequences
; CURRENT APPLICATION NUMBER: US/09/539,601C
; EARLIER FILING DATE: 2001-08-30
; EARLIER APPLICATION NUMBER: 199 15 178.4 GERMANY
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 4
; LENGTH: 8637
; TYPE: DNA
; ORGANISM: Hepatitis C virus
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)..(341)
; OTHER INFORMATION: construct I377/NS2-3'/wt
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (342)..(1181)
; OTHER INFORMATION: HCV core-neomycin phosphotransferase fusion
; OTHER INFORMATION: protein
; FEATURE:
; NAME/KEY: RBS
; LOCATION: (1190)..(1800)

OTHER INFORMATION: internal ribosome entry site from
OTHER INFORMATION: encephalomyocarditis virus

FEATURE:
NAME/KEY: CDS

LOCATION: (1801)..(8406)

OTHER INFORMATION: hepatitis C virus NS2 - 5B

FEATURE:

NAME/KEY: 3'UTR

LOCATION: (8407)..(8637)

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AUTHORS: Lohmann, Volker

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Query Match 91.6%; Score 7324.6; DB 4; Length 8637;

Best Local Similarity 92.5%; Pred. No. 0;

Matches 7985; Conservative 0; Mismatches 4; Indels 648; Gaps 1;

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QY	121	CCCCCTCCGGGAGGACATAGTGGTCTGCGGAACCGGTGAGTACACCGGAATGCCAG	180
DB	121	CCCCCTCCGGGAGGACATAGTGGTCTGCGGAACCGGTGAGTACACCGGAATGCCAG	180
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QY	241	GGGAGACTCTAGCCGAGTAGTGTGGGTGCGAAAGGCTTGTGTTACTGCTGATAGG	300
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QY	301	GTGCTTGGAGTGGCCCGGAGGTCTGTAGACCGTGCACCATGAGCAGGAATCCTAAAC	360
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DB	781	CATTTCGACCAACCAAGAGGATCGCATCGAGCGAGCAGTACTCGGATGGAAGCCGGTC	840
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DB	901	CCAGGCTCAAGCGCGCATGCGCGAGGAGTCTGCTGTCGACCATCGCGATGCT	960
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QY	1621	TGCTCTCTCAAGCTTATCAACAGGGGCTGAAGATGCCAGAGGTACCCCATTTGT	1680
DB	1621	TGCTCTCTCAAGCTTATCAACAGGGGCTGAAGATGCCAGAGGTACCCCATTTGT	1680
QY	1681	ATGGGATCTGATCTGGGCTCGGTGCAATGCTTATCATGTTTGTAGTCGAGTTAAA	1740
DB	1681	ATGGGATCTGATCTGGGCTCGGTGCAATGCTTATCATGTTTGTAGTCGAGTTAAA	1740
QY	1741	AAGCTCTAGGCCCCCGAACCGAGGAGCTGTTTCTTCAAAACACGATAATACC	1800

Db 1741 AACGCTAGGCCCCCGGAAACACGAGGACGCTGGTTCCTTTGAAAAACACGATATACC 1800
QY 1801 ATG----- 1803
Db 1801 ATGGACGGGAGATGGCAGCATCTGTCGGAGCGCGGTTTTCGTAGGTCTGATCTCTTG 1860
QY 1804----- 1803
Db 1861 ACCTGTGTCACCGCACTATAAGCTGTTCTCTGCTAGGCTCATATGTTGGTTACAATATTTT 1920
QY 1804----- 1803
Db 1921 ATCACAGGCGGAGGCACACTTGAAGTGTGGATCCCGCCCTCAACGTTTCGGGGGGGC 1980
QY 1804----- 1803
Db 1981 CGCGATGCCGTATCTCTCTCAGTTCGGGATCCACCCAGAGCTAATCTTTACCATCACC 2040
QY 1804----- 1803
Db 2041 AAAATCTTGTTCGCATACTCGTCCACTCATGTGTGCTCCAGGCTGGTATAACCAAGTG 2100
QY 1804----- 1803
Db 2101 CCGTACTTCGTGCGCGCACACGGGCTCATTCGTGCATGCTATGCTGGTTCGGAAGTTCGT 2160
QY 1804----- 1803
Db 2161 GGGGTCATTAATGTCCTCAATGGCTCTCATGAAGTTGGCCGCACTGACAGGTACGTACGTT 2220
QY 1804----- 1803
Db 2221 TATGACCATCTCACCCACTGCGGACTGCGCCACGCGGCTTACGAGACCTTCGGGTG 2280
QY 1804----- 1803
Db 2281 GCAGTGAGCCCGTCTCTCTCTGATATGGAGACCAAGTTATCATCTGGGGGGCAGAC 2340
QY 1804----- 1803
Db 2341 ACCGCGCGTGTGGGACATCATCTTGGGCTGCGCGTCTCCGCGCCGACAGGGGAGGAG 2400
QY 1804----- 1812
Db 2401 ATACATCTGGGACCGGCAGACAGCTTGAAGGGCAGGGTGGGACTCTCTCGCGCTATT 2460
QY 1813 ACAGGCTACTCCCAAGAGCGAGGCTTACTTGGCTGGATCATCACTAGCTTCACAGGC 1872
Db 2461 ACAGGCTACTCCCAAGAGCGAGGCTTACTTGGCTGGATCATCACTAGGCTTCACAGGC 2520
QY 1873 CGGACAGGAAACAGGTCGAGGGGAGTCCAGTGGTCTCCACCGCAACACATCTTTC 1932
Db 2521 CGGACAGGAAACAGGTCGAGGGGAGTCCAGTGGTCTCCACCGCAACACATCTTTC 2580
QY 1933 CTGGGACCTGCTCAATGGCGTGTGTGGACTGTCTATCATGTGCGGCTCAAGAGCC 1992
Db 2581 CTGGGACCTGCTCAATGGCGTGTGTGGACTGTCTATCATGTGCGGCTCAAGAGCC 2640
QY 1993 CTTCGCGCCCAAGGGCCCAATCACCCAAATGTACCAATGTGACACAGGACCTCGTC 2052
Db 2641 CTTCGCGCCCAAGGGCCCAATCACCCAAATGTACCAATGTGACACAGGACCTCGTC 2700
QY 2053 GGCTGCAAGCGCCCCCGGGGCGGTTCTCTGACACCATGCACTCCGCGAGCTCGGAC 2112
Db 2701 GGCTGCAAGCGCCCCCGGGGCGGTTCTCTGACACCATGCACTCCGCGAGCTCGGAC 2760
QY 2113 CTTTACTTGTTCAGAGGATCCGATGTCAATTCGGTGGCGCGGGGCGCAGACAGG 2172
Db 2761 CTTTACTTGTTCAGAGGATCCGATGTCAATTCGGTGGCGCGGGGCGCAGACAGG 2820
QY 2173 GGGAGGCTACTCTCCCGCCAGGCCCGTCTCTACTTGAAGGCTTCCTTCGGGCGGTCCACTG 2232
Db 2821 GGGAGGCTACTCTCTCCCGCCAGGCCCGTCTCTACTTGAAGGCTTCCTTCGGGCGGTCCACTG 2880

QY 2233 CTCTCCCCCTCGGGCAGCGCTGTGGGCATCTTTTCGGGCTGCGGTGTGACCCGAGGGTT 2292
Db 2881 CTCTCCCCCTCGGGCAGCGCTGTGGGCATCTTTTCGGGCTGCGGTGTGACCCGAGGGTT 2940
QY 2293 GCGAAGGCGGTGGACTTTGTACCCGTTCAGTCTATGGAACCACTATGCGGTCCCGGTC 2352
Db 2941 GCGAAGGCGGTGGACTTTGTACCCGTTCAGTCTATGGAACCACTATGCGGTCCCGGTC 3000
QY 2353 TTCAGCAACAATCTGCTCCCTCCGCGCGTACCGAGACATTCACAGTGGGCCCATCTACAC 2412
Db 3001 TTCAGCAACAATCTGCTCCCTCCGCGCGTACCGAGACATTCACAGTGGGCCCATCTACAC 3060
QY 2413 GCCCTACTGTAGCGGCAAGACACTAAGTTCGCGGTGCGGTATGACAGCCCAAGGTAT 2472
Db 3061 GCCCTACTGTAGCGGCAAGACACTAAGTTCGCGGTGCGGTATGACAGCCCAAGGTAT 3120
QY 2473 AAGGTGCTTGTCTGAAACCCGTCGTCGCGCGACCTTAGGTTCGCGGCGGTATATGTC 2532
Db 3121 AAGGTGCTTGTCTGAAACCCGTCGTCGCGCGACCTTAGGTTCGCGGCGGTATATGTC 3180
QY 2533 AAGGCATATGTTATCGACCCCTAACATCAGAACCGGGGTAAAGACCATCACACGGTGCC 2592
Db 3181 AAGGCATATGTTATCGACCCCTAACATCAGAACCGGGGTAAAGACCATCACACGGTGCC 3240
QY 2593 CCCATACGTTACTCCACTATGCAAGTTTCTTCCGACGCGTGGTGTCTCTGGGGGCGCC 2652
Db 3241 CCCATACGTTACTCCACTATGCAAGTTTCTTCCGACGCGTGGTGTCTCTGGGGGCGCC 3300
QY 2653 TATGACATCATATATGTATGATGAGTGCACCTCAACTGACTCGACCATCTCTGGGATC 2712
Db 3301 TATGACATCATATATGTATGATGAGTGCACCTCAACTGACTCGACCATCTCTGGGATC 3360
QY 2713 GGCACAGTCTCTGACCAAGCGAGACGCGCTGGAGCGGACTCTGTCGTCGTCGCGCACCGCT 2772
Db 3361 GGCACAGTCTCTGACCAAGCGAGACGCGCTGGAGCGGACTCTGTCGTCGTCGCGCACCGCT 3420
QY 2773 AGGCTCCGGATGCGTCACTGCGGCACATCCAAACATCGAGGAGTGGTCTCTGTCAGC 2832
Db 3421 AGGCTCCGGATGCGTCACTGCGGCACATCCAAACATCGAGGAGTGGTCTCTGTCAGC 3480
QY 2833 ACTGGAAATCCCTTTTATGCAAGCCATTCGCCATTCGAGACCATCAAGGGGGGAGG 2892
Db 3481 ACTGGAAATCCCTTTTATGCAAGCCATTCGCCATTCGAGACCATCAAGGGGGGAGG 3540
QY 2893 CACCTCATTTTCTGCCATTCGAAGAAATGTAGTGCCTCGCGGAGTGTTCGCGC 2952
Db 3541 CACCTCATTTTCTGCCATTCGAAGAAATGTAGTGCCTCGCGGAGTGTTCGCGC 3600
QY 2953 CTGCGACTCAATGCTGTAGCATATTAACCGGGGCTTTGATGTATCCGTCATACCAACTAGC 3012
Db 3601 CTGCGACTCAATGCTGTAGCATATTAACCGGGGCTTTGATGTATCCGTCATACCAACTAGC 3660
QY 3013 GGAGAGCTCATTTCTGTCGCAACGGAGCTCTAATGACCGGCTTTACCGGCGATTTGAC 3072
Db 3661 GGAGAGCTCATTTCTGTCGCAACGGAGCTCTAATGACCGGCTTTACCGGCGATTTGAC 3720
QY 3073 TCAGTGATCGACTGCAATACATGTGTACCCAGACAGTTCGACTTCAGCTTCGAGCCCGAGC 3132
Db 3721 TCAGTGATCGACTGCAATACATGTGTACCCAGACAGTTCGACTTCAGCTTCGAGCCCGAGC 3780
QY 3133 TTCACATTTAGACAGCAGCCGTCACAGAGCGCGGTGTACGCTTCGAGCGCGGAGGC 3192
Db 3781 TTCACATTTAGACAGCAGCCGTCACAGAGCGCGGTGTACGCTTCGAGCCCGAGC 3840
QY 3193 AGGACTGTAGGGGAGGATGGCATTTACAGTTTGTACTTCAGAGAGAAACCGGCTCG 3252
Db 3841 AGGACTGTAGGGGAGGATGGCATTTACAGTTTGTACTTCAGAGAGAAACCGGCTCG 3900
QY 3253 GGCATGTTTCTGTTCTGCTGCGAGTGTATGACCGGGGCTGTCTGTTGGTACGAG 3312
Db 3901 GGCATGTTTCTGTTCTGCTGCGAGTGTATGACCGGGGCTGTCTGTTGGTACGAG 3960

QY	3313	CTCAGCCGCGCGAGACCTCAGTTAGTTGGGGCTTACCTAAACACACAGGGTTGCCC	3372	Db	5041	GGCGCCCTAGTCGTGGGGTCTGTGGCAGCGATCTGGTCGGCAGCTGGGGCCAGGG	5100
Db	3361	CTCAGCCGCGCGAGACCTCAGTTAGTTGGGGCTTACCTAAACACACAGGGTTGCCC	4020	QY	4453	GAGGGGGTGTGAGTGAGTGAAACCGGCTGATAGGTTGCGTTCGCGGGGTAAACAGTC	4512
QY	3373	GTCTGCCAGGACCATCTGGAGTCTGGGAGAGCGTCTTTACAGGCTCACCACCATAGAC	3432	Db	5101	GAGGGGGTGTGAGTGAGTGAAACCGGCTGATAGGTTGCGTTCGCGGGGTAAACAGTC	5160
Db	4021	GTCTGCCAGGACCATCTGGAGTCTGGGAGAGCGTCTTTACAGGCTCACCACCATAGAC	4080	QY	4513	TCCCCACGCACTATGTCCTGAGAGGACGCTGCAGCACGTCGTCACTCAGATCCTCTCT	4572
QY	3433	GCCATTCTTCTGCCAGACTAAGCAGCAGGAGACAACTTCCCTCACTCTGGTAGCATAC	3492	Db	5161	TCCCCACGCACTATGTCCTGAGAGGACGCTGCAGCACGTCGTCACTCAGATCCTCTCT	5220
Db	4081	GCCATTCTTCTGCCAGACTAAGCAGCAGGAGACAACTTCCCTCACTCTGGTAGCATAC	4140	QY	4573	AGTCTTACCATCACTCAGCTCTGAAGAGGCTTCAACAGTGAGTCAACAGAGACTGTCTC	4632
QY	3493	CAGGCTACGGTGTGCCAGGCTCAGGCTCAGCTCAGCTCAGCTGCTGGGACCAATGTGAAG	3552	Db	5221	AGTCTTACCATCACTCAGCTCTGAAGAGGCTTCAACAGTGAGTCAACAGAGACTGTCTC	5280
Db	4141	CAGGCTACGGTGTGCCAGGCTCAGGCTCAGCTCAGCTCAGCTGCTGGGACCAATGTGAAG	4200	QY	4633	AGCCATCTCTCGGCTCGTGGCTAAGAGATGTTTGGGATGAGATGATGACGCTGTGACT	4692
QY	3553	TGTCTCATACGGCTAAGCCTACGCTGACGCGGCCAACGCCCTCTGTATAGGCTGGGA	3612	Db	5281	AGCCATCTCTCGGCTCGTGGCTAAGAGATGTTTGGGATGAGATGATGACGCTGTGACT	5340
Db	4201	TGTCTCATACGGCTAAGCCTACGCTGACGCGGCCAACGCCCTCTGTATAGGCTGGGA	4260	QY	4693	GATTTCAAGACTGGCTCCAGTCCAGTCCCTGCGCGCATTTGCCGGGAGTCCCTTCTTC	4752
QY	3613	GCCGTTCAAAACGAGGTTACTACACACACACCCCATACCAAAATACATATGGCATGATG	3672	Db	5341	GATTTCAAGACTGGCTCCAGTCCAGTCCCTGCGCGCATTTGCCGGGAGTCCCTTCTTC	5400
Db	4261	GCCGTTCAAAACGAGGTTACTACACACACACCCCATACCAAAATACATATGGCATGATG	4320	QY	4753	TCATGTCAACGCTGGGTACAAGGAGTCTGGCGGGGCGACGGCATCATGCAAAACCACTGC	4812
QY	3673	TGGGTGACCTGGAGTGTGACGAGCAGCTGGGTGCTGGTAGGCGGAGTCTTAGAGCT	3732	Db	5401	TCATGTCAACGCTGGGTACAAGGAGTCTGGCGGGGCGACGGCATCATGCAAAACCACTGC	5460
Db	4321	TGGGTGACCTGGAGTGTGACGAGCAGCTGGGTGCTGGTAGGCGGAGTCTTAGAGCT	4380	QY	4813	CCATGTGAGGACACATCACCAGCATGTGAAAGGTTTCCATGAGGATCGTGGGGCT	4872
QY	3733	CTGGCGCGTATGCTGACACAGGACGCTGCTCATTTGGCGAGGATCATCTGTCTC	3792	Db	5461	CCATGTGAGGACACATCACCAGCATGTGAAAGGTTTCCATGAGGATCGTGGGGCT	5520
Db	4381	CTGGCGCGTATGCTGACACAGGACGCTGCTCATTTGGCGAGGATCATCTGTCTC	4440	QY	4873	AGGACTGTAGTAAACACAGTGGCATGGAAATTTCCCATTTAAACGCGTACACCGGCCCC	4932
QY	3793	GGAAGCCGCGCATCATTTCCCGACAGGAGTCTTTACCGGAGTTCATGAGTGAAG	3852	Db	5521	AGGACTGTAGTAAACACAGTGGCATGGAAATTTCCCATTTAAACGCGTACACCGGCCCC	5580
Db	4441	GGAAGCCGCGCATCATTTCCCGACAGGAGTCTTTACCGGAGTTCATGAGTGAAG	4500	QY	4933	TGACAGCCCTCCCGCGCCAAATTTATTTAGGGCTGTGGGGGTGCTGCTGAGGAG	4992
QY	3853	GAGTGGCTCTACACCTCCCTTACATCGAACAGGAGTACGCTCGCGAAATTCATA	3912	Db	5581	TGACAGCCCTCCCGCGCCAAATTTATTTAGGGCTGTGGGGGTGCTGCTGAGGAG	5640
Db	4501	GAGTGGCTCTACACCTCCCTTACATCGAACAGGAGTACGCTCGCGAAATTCATA	4560	QY	4993	TAGCTGAGGATTCAGCGGTGGGGATTTCCACTAGTCACGGGCTATGACCTGACAAAC	5052
QY	3913	CAGAGGCAATCGGTTGCTGCAACACGACCAAGCAGGAGGCTGCTGCTCCGCTG	3972	Db	5641	TAGCTGAGGATTCAGCGGTGGGGATTTCCACTAGTCACGGGCTATGACCTGACAAAC	5700
Db	4561	CAGAGGCAATCGGTTGCTGCAACACGACCAAGCAGGAGGCTGCTGCTCCGCTG	4620	QY	5053	GTAAGTGCCGCTGTGAGGTTCCGGCCCCCGAATTTCTTACAGAAAGTGAATGGGGTGGG	5112
QY	3973	GTGGAATCCAAAGTGGCGACCTCGAAGCTTCTGGGCGAAGCATATGTGGAAATTCATC	4032	Db	5701	GTAAGTGCCGCTGTGAGGTTCCGGCCCCCGAATTTCTTACAGAAAGTGAATGGGGTGGG	5760
Db	4621	GTGGAATCCAAAGTGGCGACCTCGAAGCTTCTGGGCGAAGCATATGTGGAAATTCATC	4680	QY	5113	TTGCAACAGGTACGCTCCAGGTGCAAAACCCCTCTTACGGGAGGAGTCAATTCCTGCTC	5172
QY	4033	AGCGGATACAATATTTAGCAGCTTGTCCACTCTGCTGGCAACCCCGGATAGCATCA	4092	Db	5761	TTGCAACAGGTACGCTCCAGGTGCAAAACCCCTCTTACGGGAGGAGTCAATTCCTGCTC	5820
Db	4681	AGCGGATACAATATTTAGCAGCTTGTCCACTCTGCTGGCAACCCCGGATAGCATCA	4740	QY	5173	GGGCTCAATCAATACCTGTTGGTCCAGCTCCCATGCGAGCCGAAACCGGACGTAGCA	5232
QY	4093	CTGATGSCATTCAAGCTCTATCACCAGCCCGCTCACCACCAACATACCTCTGTTT	4152	Db	5821	GGGCTCAATCAATACCTGTTGGTCCAGCTCCCATGCGAGCCGAAACCGGACGTAGCA	5880
Db	4741	CTGATGSCATTCAAGCTCTATCACCAGCCCGCTCACCACCAACATACCTCTGTTT	4800	QY	5233	GTGCTCACTTCCATGTCTCACCGACCCCTCCCATTTACGGCGGAGACGGTAAAGCTAGG	5292
QY	4153	AACATCTGGGGGATGGGTGGCGCCAACTTGTCTCTCCAGCGCTGTCTGCTTTC	4212	Db	5881	GTGCTCACTTCCATGTCTCACCGACCCCTCCCATTTACGGCGGAGACGGTAAAGCTAGG	5940
Db	4801	AACATCTGGGGGATGGGTGGCGCCAACTTGTCTCTCCAGCGCTGTCTGCTTTC	4860	QY	5293	CTGGCAGGGGATCTCCCGCTCTTGGCCAGCTCATCAGTACGACGCTGTCTGCGCT	5352
QY	4213	GTAGGCGCGGATCTGGAGCGGCTGTTGGGAGCATAGGCTTGGGAAAGTGTCTGTG	4272	Db	5941	CTGGCAGGGGATCTCCCGCTCTTGGCCAGCTCATCAGTACGACGCTGTCTGCGCT	6000
Db	4861	GTAGGCGCGGATCTGGAGCGGCTGTTGGGAGCATAGGCTTGGGAAAGTGTCTGTG	4920	QY	5353	TCCTTTGAAGCAACATGCACTACCGCTCATGACTCCCGGACGCTGACTCATCGAGGCC	5412
QY	4273	GATATTTGGCAGGTTATGAGACAGGGGTGGCAGGCGCTGTGGCTTTAAGGTCATG	4332	Db	6001	TCCTTTGAAGCAACATGCACTACCGCTCATGACTCCCGGACGCTGACTCATCGAGGCC	6060
Db	4921	GATATTTGGCAGGTTATGAGACAGGGGTGGCAGGCGCTGTGGCTTTAAGGTCATG	4980	QY	5413	AACTCTCTGTGGCGGACAGGATGGCGGGAAACATACCCCGCTGGAGTCAAGAAATAG	5472
QY	4333	AGCGGCGAGATGCCCTCCACCGAGGACCTGCTAACCTTCTCCCTGTATCTCCCT	4392	Db	6061	AACTCTCTGTGGCGGACAGGATGGCGGGAAACATACCCCGCTGGAGTCAAGAAATAG	6120
Db	4981	AGCGGCGAGATGCCCTCCACCGAGGACCTGCTAACCTTCTCCCTGTATCTCCCT	5040	QY	5473	GTAGTAATTTGGACTCTTTCGAGCGCTCCACGCGAGGAGGATGAGAGGAAATATCC	5532
QY	4393	GGCGCCCTAGTCGTGGGGTCTGTGCGACCGATCTGCTGCGGACAGTGGGCGCAGGG	4452				

6121 GTAGTAATTTTGGACTCTTTTCAGCCGCTCCAAAGCGGAGGAGTATGAGAGGAGTATCC 6180 Db
5533 GTTCGGCGGAGATCTTCGGAGGTTCAGGAAATTCCTTCAGGCGATGCCCATATGGGCA 5592 QY
6181 GTTCGGCGGAGATCTTCGGAGGTTCAGGAAATTCCTTCAGGCGATGCCCATATGGGCA 6240 Db
5593 CGCCCGGATTACAAACCTCCACTCTTTAGAGTCTCTGGAAGGACCCGGACTACTGCTCCCTCCA 5652 QY
6241 CGCCCGGATTACAAACCTCCACTCTTTAGAGTCTCTGGAAGGACCCGGACTACTGCTCCCTCCA 6300 Db
5653 GTGGTACACGGGTGTCCATTGCCGCTGTCGAAGGCCCTCCGATPACACACTCTCCACGGAGG 5712 QY
6301 GTGGTACACGGGTGTCCATTGCCGCTGTCGAAGGCCCTCCGATPACACACTCTCCACGGAGG 6360 Db
5713 AAGGAGCGGTGTCTGCTCAGATCTACCGTGTCTTCGCTTGGCGGAGCTGCGCACCA 5772 QY
6361 AAGGAGCGGTGTCTGCTCAGATCTACCGTGTCTTCGCTTGGCGGAGCTGCGCACCA 6420 Db
5773 AAGACCTTTCGGCAGCTCCGAATCGTTCGGCCGTTCGACAGCGGCACCGCAACCGGCTCTCCT 5832 QY
6421 AAGACCTTTCGGCAGCTCCGAATCGTTCGGCCGTTCGACAGCGGCACCGCAACCGGCTCTCCT 6480 Db
5833 GACACGCTTCCGACGACGCGGATCGGATTCGAGTCGTACTCTCCATGCCCC 5892 QY
6481 GACACGCTTCCGACGACGCGGATTCGAGTCGTACTCTCCATGCCCC 6540 Db
5893 CCCCTTGAAGGGGAGCCGGGGATCCCGATCTCAGCGACGGGTCTTGCTACGTTAAGC 5952 QY
6541 CCCCTTGAAGGGGAGCCGGGGATTCGAGTCGTACTCAGCGACGGGTCTTGCTACGTTAAGC 6600 Db
5953 GAGGAGCTAGTGAGGACGTCTGCTGCTGCTGATGCTTACACATCGGACGAGCGGCCCTG 6012 QY
6601 GAGGAGCTAGTGAGGACGTCTGCTGCTGCTGATGCTTACACATCGGACGAGCGGCCCTG 6660 Db
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6721 CTCGGTCAACAACTTGGTCTATGCTTACAAATCTCGACGCGCAAGCTTCGGCGAGAAG 6780 Db
6133 AAGGTCACTTTTGACAGACTGCGAGGCTCTGACGACCACTTACCGGACGCTGCTCAAGGAG 6192 QY
6781 AAGGTCACTTTTGACAGACTGCGAGGCTCTGACGACCACTTACCGGACGCTGCTCAAGGAG 6840 Db
6193 ATGAAGCGAAGCGCTCCAGTTAAGGCTAAACTTCTATCCGTGGAGGAGCCTGTAAG 6252 QY
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6373 GAGACACCAATTGACACCACTATGCGCAAAATGAGTTTTCTGCGTCCAAACAGAG 6432 QY
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7333 TGTACTCTCATTGAGCCTTGAACCTACCTCAGATCAATCAACGACTCCATGGCCTTAGC 7392 QY
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7393 GCATTTTCACTCATAGTTACTCTCCAGGTGAGATCAATAGGTTGCTTCATGCTCAGG 7452 QY
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DB 1021 ACTGTGGCCGGCTGGGTGTGGCGACCGCTATCAGGACATAGCGTTGGCTACCGTGATA 1080
QY 1069 TTGCTGAAGAGCTTGGGGGCGAATGGGCTGACCGCTTCTCGTGTCTTACCGGTATCGCGG 1128
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QY 1129 CTCGGGATTCGACGCGATCGCCTTCTATCGCCTTCTTGACGAGTCTTCTGAGTTTAAA 1188
DB 1141 CTCGGGATTCGACGCGATCGCCTTCTATCGCCTTCTTGACGAGTCTTCTGAGTTTAAA 1200
QY 1189 CAGACCAACACGGTTTCCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCGCT 1248
DB 1201 CAGACCAACACGGTTTCCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCGCT 1260
QY 1249 AACGTTACTGGCCGACCGCTTGGAAATAGGCCGGTGTGGTTTGTCTATATGTTATTT 1308
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QY 1369 ACAGGCAATTCCTAGGGGTCTTTCCCTCTCGCCAAAGGAATGCAAGTCTGTGTAATGTC 1428
DB 1381 ACAGGCAATTCCTAGGGGTCTTTCCCTCTCGCCAAAGGAATGCAAGTCTGTGTAATGTC 1440
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DB 1441 GTGAAGAGAGCTTCTCTGGAAGCTTCTTGAAGCAAAACACGCTGTGAGCGACCTT 1500
QY 1489 TGCAAGCAGCGGAACCCCGACCTGGCGACAGTGGCTCTCGCGCCAAAAGCCACGTTGA 1548
DB 1501 TGCAAGCAGCGGAACCCCGACCTGGCGACAGTGGCTCTCGCGCCAAAAGCCACGTTGA 1560
QY 1549 TAAGATACACTCTGAAGGCGGACAAACCCAGTGCACCTGTGAGTGTGATGTTGTG 1608
DB 1561 TAAGATACACTCTGAAGGCGGACAAACCCAGTGCACCTGTGAGTGTGATGTTGTG 1620
QY 1609 GAAAGAGTCAATAGGCTCTCTCAAGCGTATCAACAAAGGGGCTGAAGGATGCCAGAAG 1668
DB 1621 GAAAGAGTCAATAGGCTCTCTCAAGCGTATCAACAAAGGGGCTGAAGGATGCCAGAAG 1680
QY 1669 GTACCCCATGTATGGATCTGATCTGGGACCTCGGTGACATGCTTTACATGTTTAG 1728
DB 1681 GTACCCCATGTATGGATCTGATCTGGGACCTCGGTGACATGCTTTACATGTTTAG 1740
QY 1729 TCGAGGTTAAAAACGCTAGGCCCCCGAAACCAACCGGACGTTGTTTCTTTGAAAAA 1788
DB 1741 TCGAGGTTAAAAACGCTAGGCCCCCGAAACCAACCGGACGTTGTTTCTTTGAAAAA 1800
QY 1789 CAGGATAATACATG----- 1803
DB 1801 CAGGATAATACATGACCGGAGATGCGAGCATCGTGGAGCGCGGTTTTTCGTAGGT 1860
QY 1804 ----- 1803
DB 1861 CTGATACTCTTGACCTTGTCACCGCATATAAGCTGTTCTCTGCTAGGCTCATATGGTGG 1920
QY 1804 ----- 1803
DB 1921 TTACATAATTTTATCACCAGGGCGGAGCACATTGCAAGTGTGGATCCCGCCCTCAAC 1980
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DB 1981 GTTGGGGGGGGCGGATGCGGTTCATCCTCTCAGTGGCGGATCCACCCAGAGCTAATC 2040
QY 1804 ----- 1803
DB 2041 TTTACCATCACCMAAATCTTGTCTGCGCATACTCGGTCCACTCATGTGTCTCCAGGCTGGT 2100

QY 1804 ----- 1803
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QY 1804 ----- 1803
DB 2161 CGGAAGGTTGTGGGGGTCAATTATGTCCAAATGGCTCTCTATGAAGTTGGCCGCACTGACA 2220
QY 1804 ----- 1803
DB 2221 GGTACGTAGGTTTATGACCATCTCACCCCACTGGGGGACTGGGCCACGCGGGCTACGA 2280
QY 1804 ----- 1803
DB 2281 GACCTTGGGTGGCAAGTTGAGCCCGTCTTCTCTGATATGGAGACCAAGGTTTATCACC 2340
QY 1804 ----- 1803
DB 2341 TGGGGGCGACACACCGCGGGGTGTGGGGACATCATCTTGGGCTGTCCCGTCTCCGCCGC 2400
QY 1804 ----- 1803
DB 2401 AGGGGAGGGAGATATCATCTGGGACCGGACAGACCTTGAAGGCGAGGGTGGCGACTC 2460
QY 1804 ----- 1860
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QY 1921 ACACAATCTTCTGGCGACTCTCGTCAATGGCGTGTGTGGACTGTCTATCATGTGTC 1980
DB 2581 ACACAATCTTCTGGCGACTCTCGTCAATGGCGTGTGTGGACTGTCTATCATGTGTC 2640
QY 1981 GGCTCAAGACCTTGGCGGCTTCCCGCCCAAGGGCCCAATCAACCAATGTACCAATGTGGAC 2040
DB 2641 GGCTCAAGACCTTGGCGGCTTCCCGCCCAAGGGCCCAATCAACCAATGTACCAATGTGGAC 2700
QY 2041 CAGGACTCTGCGGTGGCAAGCGCCCGCGGGCGGTTCCTTGACACCATGCACTGTC 2100
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DB 2941 ACCGAGGGGTTGCGAAGCGGTGGACTTTGTACCGTCTGAGTCTATGAAACCATATG 3000
QY 2341 CGGTCCCGGCTTTCACGAGCAACTCTGTCCTCCCGCGGTACCGGACATTTCCAGGTG 2400
DB 3001 CGGTCCCGGCTTTCACGAGCAACTCTGTCCTCCCGCGGTACCGGACATTTCCAGGTG 3060
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QY 2521 GCGTATATGTCTAAGGCAATGGTATCGACCCCTAAACATCAGAACCGGGGTAGGACCATC 2580

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QY 4801 CAACACACCTCCCATGTGGAGGACAGATCAACCGACATGTGAATAAAGGTTTCCATGAGG 4860
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Db ATCGTGGGGCTTAGGACCTGTAGTAACACGTCGGCATGGAACATTTCCCTCCATTAACGCGTAC 5580
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Db AGGGAAGTATCCGTTCCGGCGGAGATCTCGGAGGTCCAGGAAATTTCCCTCGAGCGATG 6240
QY 5581 CCCATATGGCGACGCGCGGATTAACCCCTCCACTGTTAGAGTCTCGGAGGATCCGAGGAG 6300
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QY 5941 TCTACCGTAAGCGAGGAGGTAGTGAGGACGCTGCTGCTGCTGATGCTCTACACATGG 6000
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QY 6421 GTCCAAACGAGAGAGGGGCGCCAGCCAGCTGCGCTTATCGTATTCAGATTTGGG 6480
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QY 6481 GTTCGTGTGTGCGAGAAATTTGCGCTTACGATGTGTCTCCACCTCCCTCAGGCGCTG 6540
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QY 6541 ATGGGCTCTTCTACCGATTCGAATCTCTCTGGAAGCGGTGCGATTCCTGTTGAAT 6600
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QY 6601 GCTGGAAGCGAGAAATTTGCGCTTACGATGTGTGCGATGACACCCGCTGTTGACTCA 6660
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QY 6721 CCGGAGCCAGACAGCCCATAGGTCGCTCAAGAGCGGCTTTACATCGGGGCGCCCTG 6780
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Db ACCAGTCCGTAATTAACCTCACTGTTTAAAGGCGCTGCGGCTGCTGAGCTGG 7560
QY 6901 AAGCTCCAGGACTGACCATGCTCGTATGCGGAGACGACCTTGTCTGTGTAAGC 6960

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DB 5247 GGGCGACAGCAGGGGAGCCTACTCTCCCGAGGCCGCTCTCCCTACTTGAAGGGCTCTTC 5306
QY 2220 GGGCGGTCCACTGCTCTCCCGCTCGGGGACGCTGTGGGCATCTTTTCGGGCTGCCGTGTG 2279
DB 5307 GGGCGGTCCACTGCTCTCCCGCTCGGGGACGCTGTGGGCATCTTTTCGGGCTGCCGTGTG 5366
QY 2280 CACCGAGGGGTTCGGAAGGGGTGGACTTTGTATCCCGTCAAGTCTATGGAACCACTAT 2339
DB 5367 CACCGAGGGGTTCGGAAGGGGTGGACTTTGTATCCCGTCAAGTCTATGGAACCACTAT 5426
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QY 2640 CTCTGGGGGCGCTATGACATCAATATATGTAGTGCCTCACTCACTGACCTCGACCAC 2699
DB 5727 CTCTGGGGGCGCTATGACATCAATATATGTAGTGCCTCACTCACTGACCTCGACCAC 5786
QY 2700 TATCTGGGCATCGGCACAGTCTCTGGACCAAGGGGAGACGGCTGGAGCGGAGCTCGTCTG 2759
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QY 2760 GCTCGCACCGCTACGGCTCGGGATCGGTCAACGTCGCCACATCCAAACATCAGGAGGT 2819
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QY 2820 GGTCTGTCTCAGCACTGGAGAAATCCCTTTTATGGCAAGCCATCCCAATCGAGACCAT 2879
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DB 5967 CAAAGGGGGAGGCACTCATTTCTGCCATTCCTCAAGAGAAATGTGATGAGCTCGCCGC 6026
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DB 6087 CATACCACTAGCGGAGAGCTCATTTCTGTAGCAACGGAGCTCTAATCAGCGGCTTTAC 6146
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DB 6207 CTTGGACCGGCTTACCATTTGAGCAGACCGGTGCCAAGACCGGTGTACGCTC 6266
QY 3180 GCAGCGGCGAGGACGACTGTGTAGGGGAGGATGGGCAATTTACAGTTGTGACTCCAGG 3239
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QY 3240 AGAACGGCCCTCGGCGATGTTTCGATTCTCGGTTCTGTGCGAGTGTATGACGCGGGCTG 3299
DB 6327 AGAACGGCCCTCGGCGATGTTTCGATTCTCGGTTCTGTGCGAGTGTATGACGCGGGCTG 6386
QY 3300 TGTCTGTGTACAGCTCAGCGCCGCGAGACCTCAGTTAGGTTGCGGCTTACCTAAACAC 3359
DB 6387 TGTCTGTGTACAGCTCAGCGCCGCGAGACCTCAGTTAGGTTGCGGCTTACCTAAACAC 6446
QY 3360 ACCAGGTTGCGGCTCTGCCAGGACCATCTCGAGTTCTGGGAGAGCCTTTTACAGGCT 3419
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QY 3600 GTATAGGCTGGAGCCGCTTCAAAACGAGGTTACTTACACACACCCCATTAACCAATACAT 3659
DB 6687 GTATAGGCTGGAGCCGCTTCAAAACGAGGTTACTTACACACACCCCATTAACCAATACAT 6746
QY 3660 CATGGCATGATGTGGCTGACCTGAGGTCGTCACGAGCACCTGGGTCGTGTAGGCGG 3719
DB 6747 CATGGCATGATGTGGCTGACCTGAGGTCGTCACGAGCACCTGGGTCGTGTAGGCGG 6806
QY 3720 AGTCTTAGAGCTCTGCGCGCTATTGCTGACAAACAGGACGCTGTCTATTGTGGCAG 3779
DB 6807 AGTCTTAGAGCTCTGCGCGCTATTGCTGACAAACAGGACGCTGTCTATTGTGGCAG 6866
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QY 3840 CGATGAGTGAAGAGTGGCGCTCACACCTTACCTTACATCGAACAGGAAATGAGCTCGC 3899
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QY 3900 CGAACAAATCAAACAGAGGCAATCGGGTTGCTGCAAAACAGCCACCAAGCAAGCGGAGGC 3959
DB 6987 CGAACAAATCAAACAGAGGCAATCGGGTTGCTGCAAAACAGCCACCAAGCAAGCGGAGGC 7046
QY 3960 TGTCTGCTCCGCTGGTGAATCCAAAGTGGCGGACCTTCGAAGCCTTCTGGCGGAAGCATAT 4019
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QY 4020 GTGGAATTTTCATCAGCGGATACAAATATTAGCAGGCTTGTCCACTCGCTGGCAACCC 4079
DB 7107 GTGGAATTTTCATCAGCGGATACAAATATTAGCAGGCTTGTCCACTCGCTGGCAACCC 7166
QY 4080 CGCGATAGCATCACTGATGGCATTCAGGCTTATCAGGCTTATCAGGCGGCTCACCAACCA 4139
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DB 7287 TGCTCTGCTTCTGCTAGCGCGCATCTGTGGAGCGGCTGTGGCAGCATAGGCTTGG 7346
QY 4260 GAAGGTCTTGTGGATATTTTGGCAGGTTATGGAGCAGGGGTGGCAGGCGCTCGTGGC 4319
DB 7347 GAAGGTCTTGTGGATATTTTGGCAGGTTATGGAGCAGGGGTGGCAGGCGCTCGTGGC 7406
QY 4320 CTTTAAAGTCTAGCGCGGAGATGCCCTCCACCGAGGACCTGGCTAACTACTCCCTGC 4379

Db	7407	CTTTAAGGTCATGAGCGCGGAGATGCCCTCCACGAGGACCTGGTTAAACCTACTTCCCTGCG	7466	8487	CCTCATCAGGCCAAACCTCTGTGGCGCAGGAGATGGCGGGGAAACATCATCCCGCGTGGA	8546
Qy	4380	TATCCTCTCCCTCGCGCGCTAGTCGTCGGGTCGTGTGCGCAGCGATATCTGCGTCGGCA	4439	5460	GTGAGAAAATAAGTAGTAATTTTGGACTCTTTTCGAGCCGCTCCCAAGCGAGGAGGATGA	5519
Db	7467	TATCCTCTCCCTCGCGCGCTAGTCGTCGGGTCGTGTGCGCAGCGATATCTGCGTCGGCA	7526	8547	GTGAGAAAATAAGTAGTAATTTTGGACTCTTTTCGAGCCGCTCCCAAGCGAGGAGGATGA	8606
Qy	4440	CGTGGGCGCAGGGGAGGGGCTGTGCAAGTGGATGAACCGGCTGTATAGCGTTTCGCTTCGCG	4499	5520	GAGGGAAGTATCCGTTTCGGCGGAGATCCTCGGAGGTCCAGGAAATTCCTCTCAGGCGAT	5579
Db	7527	CGTGGCGCCAGGGGAGGGGCTGTGCAAGTGGATGAACCGGCTGTATAGCGTTTCGCTTCGCG	7586	8607	GAGGGAAGTATCCGTTTCGGCGGAGATCCTCGGAGGTCCAGGAAATTCCTCTCAGGCGAT	8666
Qy	4500	GGGTAAACAGCTCTCCCGCAGCACTATGTGCTGAGAGCAGCGCTGAGCAGCTGTCTAC	4559	5580	GCCCATATGGGCAACGCCGGATTACAACCTCTCACTGTAGAGTCTCTGGAGGACCCGGA	5639
Db	7587	GGGTAAACAGCTCTCCCGCAGCACTATGTGCTGAGAGCAGCGCTGAGCAGCTGTCTAC	7646	8667	GCCCATATGGGCAACGCCGGATTACAACCTCTCACTGTAGAGTCTCTGGAGGACCCGGA	8726
Qy	4560	TCAGATCTCTCTAGTCTTACATCACTCAGCTGCTGAAGAGGCTTCAACAGTGGATCAA	4619	5640	CTAGCTCCCTCCAGTGTACACGGGTGTCATTCGCGCTCCCAAGGCCCTCCGATACC	5699
Db	7647	TCAGATCTCTCTAGTCTTACATCACTCAGCTGCTGAAGAGGCTTCAACAGTGGATCAA	7706	8727	CTAGCTCCCTCCAGTGTACACGGGTGTCATTCGCGCTCCCAAGGCCCTCCGATACC	8786
Qy	4620	CGAGGACTGCTCCAGCGCATGCTCCGGCTCGTGGCTAAGAGATGTTTGGGATGGATATG	4679	5700	ACCTCCAGGAGGAGGACGGTTGCTCTGTCAAGATCTTACCGTGTCTTCTGCTTGGC	5759
Db	7707	CGAGGACTGCTCCAGCGCATGCTCCGGCTCGTGGCTAAGAGATGTTTGGGATGGATATG	7766	8787	ACCTCCAGGAGGAGGACGGTTGCTCTGTCAAGATCTTACCGTGTCTTCTGCTTGGC	8846
Qy	4680	CACGCTGTGACTGATTTCAAGACCTGCTCCAGTCCAGTCCAGTCTCTGCGCGGATTCGCGG	4739	5760	GGAGTCCCAACAGACCTTCGGCAGCTCCGAATCTGCGCGCTCGACAGCGGACCGC	5819
Db	7767	CACGCTGTGACTGATTTCAAGACCTGCTCCAGTCCAGTCCAGTCTCTGCGCGGATTCGCGG	7826	8847	GGAGTCCCAACAGACCTTCGGCAGCTCCGAATCTGCGCGCTCGACAGCGGACCGC	8906
Qy	4740	AGTCCCTCTCTCTCATGCTCAACGTGGGTACAAGGAGTCTGCGCGGCGGCGAGCGGATCAT	4799	5880	CTCTCTCATGCTCCCTTTGAGGGGAGCGCGGGGATCCCGATCTCAGGACGGGTCTTG	5939
Db	7827	AGTCCCTCTCTCTCATGCTCAACGTGGGTACAAGGAGTCTGCGCGGCGGCGAGCGGATCAT	7886	8967	CTCTCTCATGCTCCCTTTGAGGGGAGCGCGGGGATCCCGATCTCAGGACGGGTCTTG	9026
Qy	4800	GCAAAACCACTGCGCATGTGGAGCAAGATCAACCGGACATGTGAAAAGGTTTCCATGAG	4859	5940	GTCTACCGTAAGCAGGAGGCTAGTGAGGACGTCTCTGCTGCTCGATGTCCTACACATG	5999
Db	7887	GCAAAACCACTGCGCATGTGGAGCAAGATCAACCGGACATGTGAAAAGGTTTCCATGAG	7946	9027	GTCTACCGTAAGCAGGAGGCTAGTGAGGACGTCTCTGCTGCTCGATGTCCTACACATG	9086
Qy	4860	GATCGTGGGCTTAGGACTGTAGTAACACGCGGATGGAACATTTCCCTCATTAACCGGTA	4919	6000	GACAGCGCCGTGATCAGCCATGCGCTGCGGAGGAAACCAAGCTGCCCATCAATGCACT	6059
Db	7947	GATCGTGGGCTTAGGACTGTAGTAACACGCGGATGGAACATTTCCCTCATTAACCGGTA	8006	9087	GACAGCGCCGTGATCAGCCATGCGCTGCGGAGGAAACCAAGCTGCCCATCAATGCACT	9146
Qy	4920	CACACGGGCGCTGACACGCCCTCCCGCGCGCAAAATTTCTAGGGCGCTGTGGCGGT	4979	6060	GAGCAACTCTTTGCTCCGTCAACCAAACTTGTGTCTATGTCTAACAATCTCGCAGCGCAAG	6119
Db	8007	CACACGGGCGCTGACACGCCCTCCCGCGCGCAAAATTTCTAGGGCGCTGTGGCGGT	8066	9147	GAGCAACTCTTTGCTCCGTCAACCAAACTTGTGTCTATGTCTAACAATCTCGCAGCGCAAG	9206
Qy	4980	GGCTGTGAGGAGTACGTGGAGGTTACCGGGTGGGGATTTCCACTAGTCAGCGGCAT	5039	6120	CCTGGCGGAGAAAGGTCACCTTTGACAGATCGCAGGTCTCTGGACACCACTTACCGGGA	6179
Db	8067	GGCTGTGAGGAGTACGTGGAGGTTACCGGGTGGGGATTTCCACTAGTCAGCGGCAT	8126	9207	CCTGGCGGAGAAAGGTCACCTTTGACAGATCGCAGGTCTCTGGACACCACTTACCGGGA	9266
Qy	5040	GACCACTGACAACTGAAAGTCCCGTTCAGGTTCCCGGCCCGCAATTTCTCACAGAAT	5099	6180	CGTGTCTCAAGGAGATGAAGCGGAAAGCGTCCACAGTTAAGGCTAAATCTTATCCGTGGA	6239
Db	8127	GACCACTGACAACTGAAAGTCCCGTTCAGGTTCCCGGCCCGCAATTTCTCACAGAAT	8186	9267	CGTGTCTCAAGGAGATGAAGCGGAAAGCGTCCACAGTTAAGGCTAAATCTTATCCGTGGA	9326
Qy	5100	GGATGGGTCGCGTGTGACAGGTPACGCTCCAGCGTGCAACCCCTCTACCGGAGGAGT	5159	6240	GGAAGCTGTAAAGTGTACGCCCGCCCAATTCGCGCAGATCTAAATTTTGGCTATGGGGCAA	6299
Db	8187	GGATGGGTCGCGTGTGACAGGTPACGCTCCAGCGTGCAACCCCTCTACCGGAGGAGT	8246	9327	GGAAGCTGTAAAGTGTACGCCCGCCCAATTCGCGCAGATCTAAATTTTGGCTATGGGGCAA	9386
Qy	5160	CACATTCCTGTCGGCTCAATCAATACCTGTTGGTTCACAGCTCCCATGCGAGCCCGA	5219	6300	GGAGCTCCGGAACCTATCAGCAAGCGGTTAAACCACTCCGCTCCGCTGTGGAAGGACTT	6359
Db	8247	CACATTCCTGTCGGCTCAATCAATACCTGTTGGTTCACAGCTCCCATGCGAGCCCGA	8306	9387	GGAGCTCCGGAACCTATCAGCAAGCGGTTAAACCACTCCGCTCCGCTGTGGAAGGACTT	9446
Qy	5220	ACCGGACGTAGGAGTGTCACTTCCATGCTCAACGACCCCTCCCAATTAACGCGGAGAC	5279	6360	GCTGGAAGACACTGAGACACCAATTTGACACCACTCATGGGCAAAAATAGAGTTTCTG	6419
Db	8307	ACCGGACGTAGGAGTGTCACTTCCATGCTCAACGACCCCTCCCAATTAACGCGGAGAC	8366	9447	GCTGGAAGACACTGAGACACCAATTTGACACCACTCATGGGCAAAAATAGAGTTTCTG	9506
Qy	5280	GGCTAAGCGTGTGCTGCGGAGGATCTCCCGCTCTTGGCGAGCTCATCAGTAGCCA	5339	6420	CGTCCAAACAGAAAGGGGGCGGAGCAGCTCCCTTATCGTATTCCTCCAGATTGGG	6479
Db	8367	GGCTAAGCGTGTGCTGCGGAGGATCTCCCGCTCTTGGCGAGCTCATCAGTAGCCA	8426	9507	CGTCCAAACAGAAAGGGGGCGGAGCAGCTCCCTTATCGTATTCCTCCAGATTGGG	9566
Qy	5340	GCTGTCTGCGCTTCTTTGAGGCAACATGCACTACCGCTCATGCTCCCGGAGCGTGA	5399	6480	GCTTCTGTGTGCGAGAAAATGGCCCTTTTACGATGTGCTTCAACCTCTCCCTCAGGCGGT	6539
Db	8427	GCTGTCTGCGCTTCTTTGAGGCAACATGCACTACCGCTCATGCTCCCGGAGCGTGA	8486	9567	GGTTCGTGTGTGCGAGAAAATGGCCCTTTTACGATGTGCTTCAACCTCTCCCTCAGGCGGT	9626

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DB 10587 TGTCGCGCTAGGCTACTGTCCAGGGGGGGCTGCCACTTGTGGAAGTACCTCTT 10646
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DB 11067 CAGATCAAGT 11076

RESULT 9
US-09-539-601-25
; Sequence 25, Application US/09539601C
; Patent No. 6630343
; GENERAL INFORMATION:
; APPLICANT: Bartschlag, Ralf FW
; TITLE OF INVENTION: Hepatitis C Virus Cell Culture System
; FILE REFERENCE: all sequences
; CURRENT APPLICATION NUMBER: US/09/539,601C
; CURRENT FILING DATE: 2001-08-30
; EARLIER APPLICATION NUMBER: 199 15 178.4 GERMANY
; EARLIER FILING DATE: 1999-04-03
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 11076
; TYPE: DNA
; ORGANISM: Hepatitis C virus
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)..(341)
; OTHER INFORMATION: construct I389/Core-3'/5.1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (342)..(1193)
; OTHER INFORMATION: hepatitis C virus core - neomycin
; OTHER INFORMATION: phosphotransferase fusion protein
; FEATURE:
; NAME/KEY: RBS
; LOCATION: (1202)..(1812)
; OTHER INFORMATION: internal ribosome entry site from
; OTHER INFORMATION: encephalomyocarditis virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1813)..(10845)
; OTHER INFORMATION: hepatitis C virus polyprotein from core to
; OTHER INFORMATION: nonstructural protein NS5B, carries cell
; OTHER INFORMATION: culture-adaptive mutations of clone 5.1
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: (10846)..(11076)
US-09-539-601-25

Query Match

77.1%; Score 6162.8; DB 4; Length 11076;

Best Local Similarity 99.7%; Pred. No. 0; Matches 6173; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 1800 CATGGCGCTATTACGGCTACTCCCAACAGACGCGAGGCTACTTGGTGCATCATCAC 1859
Db 4887 CTTGGCGCTATTACGGCTACTCCCAACAGACGCGAGGCTACTTGGTGCATCATCAC 4946
QY 1860 TAGCCTCAGAGCGCGGACAGAAACAGGTCGAGGGGAGGTCCAGGTGCTCTCCACGGC 1919
Db 4947 TAGCCTCAGAGCGCGGACAGAAACAGGTCGAGGGGAGGTCCAAAGTGGTCTCCACGGC 5006
QY 1920 AACCAATCTTCTGGGACCTCGCTCAATGGGCTGTGGTGGACTGCTATCATGTGTC 1979
Db 5007 AACCAATCTTCTGGGACCTCGCTCAATGGGCTGTGGTGGACTGCTATCATGTGTC 5066
QY 1980 CGGCTCAAGACCTTTCGGCGCCCAAGGGGCCCAATCAACCAATGTATACCAATGTGGA 2039
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QY 2040 CCAGGACCTCGTGGCTGGCAAGCGCCCGCGGGCGGTTCTTGACACCATGCACCTG 2099
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QY 2100 CGGAGCTCGACCTTTACTTGTGTACAGGCGATCCGATGTCTATCCGCTGCGCGGCG 2159
Db 5187 CGGAGCTCGACCTTTACTTGTGTACAGGCGATCCGATGTCTATCCGCTGCGCGGCG 5246
QY 2160 GGGCGACAGCGGGGAGCTACTCTCCCGAGGCGGCTCTCTACTTGAAGGGCTCTTC 2219
Db 5247 GGGCGACAGCGGGGAGCTACTCTCCCGAGGCGGCTCTCTACTTGAAGGGCTCTTC 5306
QY 2220 GGGCGGTCCACTGCTCTGCGCTCGGGGACGCTGTGGGCATCTTTCGGGCTGCGGTG 2279
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Db 5367 CACCGAGGGTGGAAAGGGGTGGACTTGTGTACCGCTCGAGTCTATGGAAACCACTAT 5426
QY 2340 GGGTCCCGGCTTTCAAGGCAAACTCGTCCCTCGGCGGTACCGGAGACATTCAGGT 2399
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Db 9387 GGAAGCTGTGAAGCTGAGCGCGGCTTAACACATCCGCTCCGCTGCTGGAAGGACTT 9446
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Db 10827 TCTACTCCCCAACCGATGAACGGGAGCTAAACACTCCAGGCAATAGGCACTCTGTT 10886
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Db 10887 TTTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 10946
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Qy 7980 CAGATCAAGT 7989
Db 11067 CAGATCAAGT 11076

RESULT 10
US-09-539-601-19
; Sequence 19, Application US/09539601C
; Patent No. 6630343
; GENERAL INFORMATION:
; APPLICANT: Bartenschlager, Ralf FW
; TITLE OF INVENTION: Hepatitis C Virus Cell Culture System
; FILE REFERENCE: all sequences
; CURRENT APPLICATION NUMBER: US/09/539,601C
; EARLIER FILING DATE: 2001-08-30
; EARLIER APPLICATION NUMBER: 199 15 178.4 GERMANY
; EARLIER FILING DATE: 1999-04-03
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 11076
; TYPE: DNA
; ORGANISM: Hepatitis C virus

FEATURE:
NAME/KEY: 5' UTR
LOCATION: (1) .. (341)
OTHER INFORMATION: construct 1389/Core-3'/9-13F
FEATURE:
NAME/KEY: CDS
LOCATION: (342) .. (1193)
OTHER INFORMATION: hepatitis C virus core - neomycin
OTHER INFORMATION: phosphotransferase fusion protein
FEATURE:
NAME/KEY: RBS
LOCATION: (1202) .. (1812)
OTHER INFORMATION: internal ribosome entry site from
OTHER INFORMATION: encephalomyocarditis virus
FEATURE:
NAME/KEY: CDS
LOCATION: (1813) .. (10845)
OTHER INFORMATION: hepatitis C virus polyprotein from core to
OTHER INFORMATION: nonstructural protein NS5B; carries cell
OTHER INFORMATION: culture-adaptive mutations from clone 9-13F
FEATURE:
NAME/KEY: 3' UTR
LOCATION: (10846) .. (11076)
US-09-539-601-13

Query Match
Best Local Similarity 77.1%; Score 6161.2; DB 4; Length 11076;
Matches 6172; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY	1800	CATGGCGCCCTATTACGGCCCTACTCCCAACAGACGCGAGGCTACTTGGCTGCATCATCAC	1859
Db	4887	CCTCGCGCCCTATTACGGCCCTACTCCCAACAGACGCGAGGCTACTTGGCTGCATCATCAC	4946
QY	1860	TAGCCTCACAGGCGCGACAGGACAGGTCGAGGGGAGGTCAGGTGCTCTCCACCGC	1919
Db	4947	TAGCCTCACAGGCGCGACAGGACAGGTCGAGGGGAGGTCAGGTGCTCTCCACCGC	5006
QY	1920	AACACAATCTTCTGGCGACCTGCGCTCAATGGCGTGTGTGGACTCTCTATCATGTGC	1979
Db	5007	AACACAATCTTCTGGCGACCTGCGCTCAATGGCGTGTGTGGACTCTCTATCATGTGC	5066
QY	1980	CGGCTCAAGACCCCTTGGCGGCGCAAGGCGCCCAATCACCCAAATGTACACCAATGTGGA	2039
Db	5067	CGGCTCAAGACCCCTTGGCGGCGCAAGGCGCCCAATCACCCAAATGTACACCAATGTGGA	5126
QY	2040	CCAGGACCTCGTGGCTGGCAAGCGCCCGCGGCGCGTTCCTTGACACCATGCACTTG	2099
Db	5127	CCAGGACCTCGTGGCTGGCAAGCGCCCGCGGCGCGTTCCTTGACACCATGCACTTG	5186
QY	2100	CGGACGCTCGGACCTTTACTTGGTCAAGGCGCATGCGGATGCTATTCGGGTGCGCGCGG	2159
Db	5187	CGGACGCTCGGACCTTTACTTGGTCAAGGCGCATGCGGATGCTATTCGGGTGCGCGCGG	5246
QY	2160	GGGCGACAGCGGGGAGGCTACTCTCCCGACGCGCGTCTCTACTTGAAGGGCTCTTC	2219
Db	5247	GGGCGACAGCGGGGAGGCTACTCTCCCGACGCGCGTCTCTACTTGAAGGGCTCTTC	5306
QY	2220	GGGCGGTCCACTGCTCTGCCCTCGGCGGACGCTGTGGGCTCTTTTCGGGCTGCCGTG	2279
Db	5307	GGGCGGTCCACTGCTCTGCCCTCGGCGGACGCTGTGGGCTCTTTTCGGGCTGCCGTG	5366
QY	2280	CAACCGAGGGTGGGAAGCGGTGGACTTTGTACCCGTCGAGTCTATGGAAACCACTAT	2339
Db	5367	CAACCGAGGGTGGGAAGCGGTGGACTTTGTACCCGTCGAGTCTATGGAAACCACTAT	5426
QY	2340	CGGTCCTCCGCTCTTACCGCACTCTGTCCTCCCTCGGCGCGTACCGCAGACATTCAGGT	2399
Db	5427	CGGTCCTCCGCTCTTACCGCACTCTGTCCTCCCTCGGCGCGTACCGCAGACATTCAGGT	5486
QY	2400	GGCCCATCTACAGCCCTTACTGCTAGCGGAGAGCACTAAGGTGCGGCTGCGGTATGC	2459
Db	5487	GGCCCATCTACAGCCCTTACTGCTAGCGGAGAGCACTAAGGTGCGGCTGCGGTATGC	5546

QY	2460	AGCCCAAGGGTATAAGGTGCTTGTCTGAAACCCGTCCTGCGCGCCACCCCTAGGTTTCGG	2519
Db	5547	AGCCCAAGGGTATAAGGTGCTTGTCTGAAACCCGTCCTGCGCGCCACCCCTAGGTTTCGG	5606
QY	2520	GGCGTATATGCTAAAGGCACATGATCGACCTTAACATCAGAACCGGGGTAAAGACCAT	2579
Db	5607	GGCGTATATGCTAAAGGCACATGATCGACCTTAACATCAGAACCGGGGTAAAGACCAT	5666
QY	2580	CACCACGGGTGCCCCCATACGTTACTCCACCTATGGCAAGTTTCTTGGCGAGCGGTGGTG	2639
Db	5667	CACCACGGGTGCCCCCATACGTTACTCCACCTATGGCAAGTTTCTTGGCGAGCGGTGGTG	5726
QY	2640	CTCTGGGGGCGCCTATGACATCATATATGTAGTGACCTCAACTGACTGCACAC	2699
Db	5727	CTCTGGGGGCGCCTATGACATCATATATGTAGTGACCTCAACTGACTGCACAC	5786
QY	2700	TATCTTGGGATCGGCACAGTCCTGGACCAAGCGGAGACGCTGAGGGCGACTCGTGT	2759
Db	5787	TATCTTGGGATCGGCACAGTCCTGGACCAAGCGGAGACGCTGAGGGCGACTCGTGT	5846
QY	2760	GTCGCGCACCGCTACGCTCCGGGATCGGTACCGTCCACATCAAAACATCGAGGAGGT	2819
Db	5847	GTCGCGCACCGCTACGCTCCGGGATCGGTACCGTCCACATCAAAACATCGAGGAGGT	5906
QY	2820	GGCTCTGTCAGCACTCGAGAAATCCCTTTTATGGCAAGCCATCCCCATCGAGACCAT	2879
Db	5907	GGCTCTGTCAGCACTCGAGAAATCCCTTTTATGGCAAGCCATCCCCATCGAGACCAT	5966
QY	2880	CAAGGGGGGAGGACCTCAATTTCTGCCATTCACGAAGAAATGTCATGAGCTCGCGC	2939
Db	5967	CAAGGGGGGAGGACCTCAATTTCTGCCATTCACGAAGAAATGTCATGAGCTCGCGC	6026
QY	2940	GAAGCTGTCCGGCTCGGACTCAATGCTGTAGCATATTTACCGGGGCTTGTATGATCCGT	2999
Db	6027	GAAGCTGTCCGGCTCGGACTCAATGCTGTAGCATATTTACCGGGGCTTGTATGATCCGT	6086
QY	3000	CATACCAACTAGCGGAGACGTCATTTGCTGTAGCAACCGGACGCTCTAATGACGGGCTTAC	3059
Db	6087	CATACCAACTAGCGGAGACGTCATTTGCTGTAGCAACCGGACGCTCTAATGACGGGCTTAC	6146
QY	3060	CGGCGATTTGCACTCAGTGTGACTGCAATCATGTCAGCATATTTACCGGGGCTTGTATGATCCGT	3119
Db	6147	CGGCGATTTGCACTCAGTGTGACTGCAATCATGTCAGCATATTTACCGGGGCTTGTATGATCCGT	6206
QY	3120	CTTGGACCGGACCTTCAATTTGAGACGACGACCGGTGCCACAAAGCGGCTGCACGCTC	3179
Db	6207	CTTGGACCGGACCTTCAATTTGAGACGACGACCGGTGCCACAAAGCGGCTGCACGCTC	6266
QY	3180	GCAGCGGCGGAGGACGACTGTAGGGGAGGATGGGCAATTTACAGGTTTGTGACTCCAGG	3239
Db	6267	GCAGCGGCGGAGGACGACTGTAGGGGAGGATGGGCAATTTACAGGTTTGTGACTCCAGG	6326
QY	3240	AGAACCGGCTCGGGCATGTTGATTCCTCGGTTCTGTGCGAGTGTATGACGCGGGCTG	3299
Db	6327	AGAACCGGCTCGGGCATGTTGATTCCTCGGTTCTGTGCGAGTGTATGACGCGGGCTG	6386
QY	3300	TGCTTGGTACGAGCTCAACCGCGCGGAGACCTCAGTTAGGTTTGGGGCTTACCTAAACAC	3359
Db	6387	TGCTTGGTACGAGCTCAACCGCGCGGAGACCTCAGTTAGGTTTGGGGCTTACCTAAACAC	6446
QY	3360	ACCAGGTTGCGGCTGCGCAGACCATCTGAGTTCTGGGAGAGGCTCTTTACAGGCT	3419
Db	6447	ACCAGGTTGCGGCTGCGCAGACCATCTGAGTTCTGGGAGAGGCTCTTTACAGGCT	6506
QY	3420	CACCCACATAGACGCGCCATTTCTTGTCCAGACTAAGCAGGCGAGGACCACTCCCTA	3479
Db	6507	CACCCACATAGACGCGCCATTTCTTGTCCAGACTAAGCAGGCGAGGACCACTCCCTA	6566
QY	3480	CTGTGTAGCATACAGGCTACGGTGTGCGCCAGGCTCAGGCTCCACCTCCATCGTGGGA	3539
Db	6567	CTGTGTAGCATACAGGCTACGGTGTGCGCCAGGCTCAGGCTCCACCTCCATCGTGGGA	6626
QY	3540	CCAAATGTGGAAGTCTCTCATACGGCTAAAGCTACGCTGACGCGGCGCAACGCCCCCTGCT	3599

Db	6627	CCAAATGTGGAGTGTCTCATACGGCTAAAGCCCTACGCTGACGGGGCAACGCCCCCTGCT	7707	CGAGGACTGCTCCACGCCATGCTCCGGCTCGTGGCTAAGAGATGTTTGGGATTGGATATG	7766
Qy	3600	GTATAGGCTGGAGCGGTTCAAAACGAGGTTACTACACACACACACCCCAATAACAT	4680	CACGGTGTGACTGATTTTCAAGACCTGGCTCCAGTCCAAAGCTCTCCGCGGATTCGCGGG	4739
Db	6687	GTATAGGCTGGAGCGGTTCAAAACGAGGTTACTACACACACACCCCAATAACAT	7767	CACGGTGTGACTGATTTTCAAGACCTGGCTCCAGTCCAAAGCTCTCCGCGGATTCGCGGG	7826
Qy	3660	CATGGCATGATGTGGCTGACCTGGAGGTCGTCAACGAGCACCTGGGTGCTGGTAGGCGG	4740	AGTCCCTCTTCTTCATGTCAAAGTGGGTAAAGGGAGTCTGGCGGGGCGACGGCATCAT	4799
Db	6747	CATGGCATGATGTGGCTGACCTGGAGGTCGTCAACGAGCACCTGGGTGCTGGTAGGCGG	7827	AGTCCCTCTTCTTCATGTCAAAGTGGGTAAAGGGAGTCTGGCGGGGCGACGGCATCAT	7886
Qy	3720	AGTCTAGACGCTGTGGCGGCTATTCTGCACACAGCAGCGGTGTCATTGTGGGCGAG	4800	GCAAAACCACTGCCCATGTGGAGCACAGATCACCGGACATGTGAAAAAGGTTTCATGAG	4859
Db	6807	AGTCTAGACGCTGTGGCGGCTATTCTGCACACAGCAGCGGTGTCATTGTGGGCGAG	7887	GCAAAACCACTGCCCATGTGGAGCACAGATCACCGGACATGTGAAAAAGGTTTCATGAG	7946
Qy	3780	GATCATCTTGTCCGGAAGCGCGGCATCATTTCCCGACAGGGAAGTCTTTTACCGGGAGTT	4860	GATCGTGGGCTTAGGACCTGTAGTAACAGCTGGCATGGAACATTTCCCAATTAAACCGCTA	4919
Db	6867	GATCATCTTGTCCGGAAGCGCGGCATCATTTCCCGACAGGGAAGTCTTTTACCGGGAGTT	7947	GATCGTGGGCTTAGGACCTGTAGTAACAGCTGGCATGGAACATTTCCCAATTAAACCGCTA	8006
Qy	3840	CGATGAGATGGAAGTGGCTCTACACCTCCCTTTACATCGAAAGGGAATGACGCTCGC	4920	CACCAACGCGCCCTGACGCGCTCCCGCGCGCCAAATTTATTCTAGGGCGCTGTGGCGGGT	4979
Db	6927	CGATGAGATGGAAGTGGCTCTACACCTCCCTTTACATCGAAAGGGAATGACGCTCGC	8007	CACCAACGCGCCCTGACGCGCTCCCGCGCGCCAAATTTATTCTAGGGCGCTGTGGCGGGT	8066
Qy	3900	CGAAACAATCAACAGAGGCAATCGGTTGCTGCAACAGCCACCAAGCAGCGAGGC	4980	GGCTGCTGAGGAGTACGTGGAGGTTTACCGGGTGGGGATTTTCCACTAGCTGACGGGCAT	5039
Db	6987	CGAAACAATCAACAGAGGCAATCGGTTGCTGCAACAGCCACCAAGCAGCGAGGC	8067	GGCTGCTGAGGAGTACGTGGAGGTTTACCGGGTGGGGATTTTCCACTAGCTGACGGGCAT	8126
Qy	3960	TGCTCTCCCGTGTGGGAATCAAGTGGCGGACCTCGAAGCTTCTGGCGGAACATAT	5040	GACCACTGACAACTGTAAGTCCCGTGTGAGTTCGCGCCCGGAAATTTCTTACAGAAAGT	5099
Db	7047	TGCTCTCCCGTGTGGGAATCAAGTGGCGGACCTCGAAGCTTCTGGCGGAACATAT	8127	GACCACTGACAACTGTAAGTCCCGTGTGAGTTCGCGCCCGGAAATTTCTTACAGAAAGT	8186
Qy	4020	GTGGAAATTTCAACGCGGATACAAATTTAGCAGGTTGTCCACTCTGCTGGCGGAACCC	5100	GGATGGGCTGGGTTGCAAGTACGCTCCAGCGTGCAGGTCGCAAAACCCCTCTTACGGGAGAGT	5159
Db	7107	GTGGAAATTTCAACGCGGATACAAATTTAGCAGGTTGTCCACTCTGCTGGCGGAACCC	8187	GGATGGGCTGGGTTGCAAGTACGCTCCAGCGTGCAGGTCGCAAAACCCCTCTTACGGGAGAGT	8246
Qy	4080	CGCGATGACATCACTGATGGGATTTACAGGCTTTGTCAGGCTTGTCCACTCTGCTGGCGGAACCC	5160	CACATTCCTGTGTGGGCTCAATCAATACCTGTGGTGGTGCAGCTCCCATGCGAGCCGA	5219
Db	7167	CGCGATGACATCACTGATGGGATTTACAGGCTTTGTCAGGCTTGTCCACTCTGCTGGCGGAACCC	8247	CACATTCCTGTGTGGGCTCAATCAATACCTGTGGTGGTGCAGCTCCCATGCGAGCCGA	8306
Qy	4140	TACCTCTCTGTTTAAATCTCTGGGGGATGGGTGGCGGCCCAACTTGTCTCTCCAGCGC	5220	ACCGAGCTGAGGCTGCTACCTTCCATGCTCACCGACCCCTCCCATATTACCGCGGAGAC	5279
Db	7227	TACCTCTCTGTTTAAATCTCTGGGGGATGGGTGGCGGCCCAACTTGTCTCTCCAGCGC	8307	ACCGAGCTGAGGCTGCTACCTTCCATGCTCACCGACCCCTCCCATATTACCGCGGAGAC	8366
Qy	4200	TGCTTCTGCTTTCGTAGGCGCGGATTCGCTGAGCGGCTGTGGAGCATAGGCTTGG	5280	GGCTAAGGCTAGGCTGGCGAGGGGATCTCCCGCTCTTGGCCAGCTCATAGCTAGCCCA	5339
Db	7287	TGCTTCTGCTTTCGTAGGCGCGGATTCGCTGAGCGGCTGTGGAGCATAGGCTTGG	8367	GGCTAAGGCTAGGCTGGCGAGGGGATCTCCCGCTCTTGGCCAGCTCATAGCTAGCCCA	8426
Qy	4260	GAGGCTGCTTGTGATTTTTCGAGGTTATGGAGCAGGGTGGCAGCGCGCTCGTGGC	5340	GCTGTCTGCGCTTCTTGAAGGCAACATGCTACCTACCGCTGATGCTCCCGGACGCTGA	5399
Db	7347	GAGGCTGCTTGTGATTTTTCGAGGTTATGGAGCAGGGTGGCAGCGCGCTCGTGGC	8427	GCTGTCTGCGCTTCTTGAAGGCAACATGCTACCTACCGCTGATGCTCCCGGACGCTGA	8486
Qy	4320	CTTTAAGTTCATGAGCGCGAGATGCCCTCCACCGAGGACCTGGCTTAACTACTCCCTGC	5400	CCTCATCGAGGCAACCTCTCTGGCGGAGGATGGCGGGGAAACATCACCGCGTGA	5459
Db	7407	CTTTAAGTTCATGAGCGCGAGATGCCCTCCACCGAGGACCTGGCTTAACTACTCCCTGC	8487	CCTCATCGAGGCAACCTCTCTGGCGGAGGATGGCGGGGAAACATCACCGCGTGA	8546
Qy	4380	TATCTCTCCCTGGCGCCCTAGTCTGGGGTGTGCGGACGATATGCTGGCGGCA	5460	GTCAAGAAAATAAGGTAGTAAATTTTGGACTCTTTCGAGCGCTTCCAAAGCGGAGGATGA	5519
Db	7467	TATCTCTCCCTGGCGCCCTAGTCTGGGGTGTGCGGACGATATGCTGGCGGCA	8547	GTCAAGAAAATAAGGTAGTAAATTTTGGACTCTTTCGAGCGCTTCCAAAGCGGAGGATGA	8606
Qy	4440	CGTGGGCGCAGGGGCGGCTGTGCAATGGATGAAACCGGCTCATAGCGTTCCCTTCGCG	5520	GAGGGAAGTATCGGTTCCCGCGGAGATCTCGGAGGTCAGGAAATTCCTTCGAGCGAT	5579
Db	7527	CGTGGGCGCAGGGGCGGCTGTGCAATGGATGAAACCGGCTCATAGCGTTCCCTTCGCG	8607	GAGGGAAGTATCGGTTCCCGCGGAGATCTCGGAGGTCAGGAAATTCCTTCGAGCGAT	8666
Qy	4500	GGGTAAACCAAGCTCTCCCAACGACATATGTGCTGAGAGGACGCTGCGACAGTGTAC	5580	GCCCATATGGGACGCGCGGATTTACAAACCTCCACTGTTTAGAGTCTCTGGAAGACCCGA	5639
Db	7587	GGGTAAACCAAGCTCTCCCAACGACATATGTGCTGAGAGGACGCTGCGACAGTGTAC	8667	GCCCATATGGGACGCGCGGATTTACAAACCTCCACTGTTTAGAGTCTCTGGAAGACCCGA	8726
Qy	4560	TCAGATCTCTCTAGTCTTACATCACTCAGCTGCTGAGAGGCTTCCACAGTGGATCAA	5640	CTACGTCCTTCCAGTGGTACAAGGTTGTCATTTGCGCGCTGCAAGGCGCTTCCGATACC	5699
Db	7647	TCAGATCTCTCTAGTCTTACATCACTCAGCTGCTGAGAGGCTTCCACAGTGGATCAA	8727	CTACGTCCTTCCAGTGGTACAAGGTTGTCATTTGCGCGCTGCAAGGCGCTTCCGATACC	8786
Qy	4620	CGAGGACTGCTCCACGCGCATGCTCCGGCTCGTGGCTTAAAGATGTTTGGGATTTGGATATG	5700	ACCTCCACGGAAGGAGGAGCGGTTCTCTGTCAGAAATCTACCGTGTCTTCTGCTTGGC	5759
			8787	ACCTCCACGGAAGGAGGAGCGGTTCTCTGTCAGAAATCTACCGTGTCTTCTGCTTGGC	8846

Db	11007	CTAGCTGAAAGTCCGTGAGCGCGTGTGACTGCAGAGAGTGTCTGATACTGGCCTCTCTG	11066
Qy	7980	CAGATCAAGT 7989	
Db	11067	CAGATCAAGT 11076	
RESULT 11			
US-09-539-601-31			
; Sequence 31, Application US/09539601C			
; Patent No. 6630343			
; GENERAL INFORMATION:			
; APPLICANT: Bartenschlager, Ralf FW			
; TITLE OF INVENTION: Hepatitis C Virus Cell Culture System			
; FILE REFERENCE: all sequences			
; CURRENT APPLICATION NUMBER: US/09/539,601C			
; CURRENT FILING DATE: 2001-08-30			
; EARLIER APPLICATION NUMBER: 199 15 178.4 GERMANY			
; EARLIER FILING DATE: 1999-04-03			
; NUMBER OF SEQ ID NOS: 51			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 31			
; LENGTH: 11076			
; TYPE: DNA			
; ORGANISM: Hepatitis C virus			
; FEATURE:			
; NAME/KEY: 5'UTR			
; LOCATION: (1)..(341)			
; OTHER INFORMATION: construct I389/Core-3'/19			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (342)..(1193)			
; OTHER INFORMATION: hepatitis C virus core - neomycin			
; OTHER INFORMATION: phosphotransferase fusion protein			
; FEATURE:			
; NAME/KEY: RBS			
; LOCATION: (1202)..(1812)			
; OTHER INFORMATION: internal ribosome entry site from			
; OTHER INFORMATION: encephalomyocarditis virus			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (1813)..(10845)			
; OTHER INFORMATION: hepatitis C virus polyprotein from core to			
; OTHER INFORMATION: nonstructural protein NS5B; carries cell culture			
; OTHER INFORMATION: adaptive mutations from clone no. 19			
; FEATURE:			
; NAME/KEY: 3'UTR			
; LOCATION: (10846)..(11076)			
US-09-539-601-31			
Query Match			
Best Local Similarity 99.6%; Pred. No. 0;			
Matches 6168; Conservative 0; Mismatches 22; Indels 0; Gaps 0;			
Qy	1800	CATGGCGCCTATTACGGCCTACTCCACAGACGGAGGCTACTTGGCTGCATCATCAC	1959
Db	4887	CCTCGCGCCTATTACGGCCTACTCCACAGACGGAGGCTACTTGGCTGCATCATCAC	4946
Qy	1860	TAGCCTCACAGGCGGACAGGAACAGGTCCAGGGGGAGGTCCAGGTGCTTCCACCGC	1919
Db	4947	TAGCCTCACAGGCGGACAGGAACAGGTCCAGGGGGAGGTCCAAAGTGTCTCCACCGC	5006
Qy	1920	AACACAATTTCTTGGCGACCTGCGTCATATGGCGTGTGTGGACTGTCTATCATGTGC	1979
Db	5007	AACACAATTTCTTGGCGACCTGCGTCATATGGCGTGTGTGGACTGTCTATCATGTGC	5066
Qy	1980	CGSCTCAAGACCCCTTCGCGGCCCAAGGCCCAATCACCAATGTACACCAATGTGA	2039
Db	5067	CGSCTCAAGACCCCTTCGCGGCCCAAGGCCCAATCACCAATGTACACCAATGTGA	5126
Qy	2040	CCAGGACCTGTCGGCTGGCAAGCGCCCGCGGCGCGTTCCTTTGACACCATGACCTG	2099

5127	CCAGGACCTCGTGGCTGGCAAGCGCCCGCGGGCGCGTTCCTTTGACACATGACACTG	5186
2100	CGGAGCTCGGACCTTTACTTTGGTCAGAGGCATCGCATGTCTATTCGGTGCCTCGCGC	2159
5187	CGGAGCTCGGACCTTTACTTTGGTCAGAGGCATCGCATGTCTATTCGGTGCCTCGCGC	5246
2160	GGGCGACAGAGGGGGAGCCCTACTCTCCCCCAGGCCCGTCTCTTCTTGAAGGCTCTTC	2219
5247	GGGCGACAGAGGGGGAGCCCTACTCTCCCCCAGGCCCGTCTCTTCTTGAAGGCTCTTC	5306
2220	GGGCGGTCACCTGCTGCTGCCCCCTCGGGGACGCTGTGGGCATCTTTGGGGTCCGGTGTG	2279
5307	GGGCGGTCACCTGCTGCTGCCCCCTCGGGGACGCTGTGGGCATCTTTGGGGTCCGGTGTG	5366
2280	CACCGAGGGGTTCGGAGGCGGTGGCTTTGTGTACCGTTCAGTCTATGGAACACCATAT	2339
5367	CACCGAGGGGTTCGGAGGCGGTGGCTTTGTGTACCGTTCAGTCTATGGAACACCATAT	5426
2340	GCGGTCCCGGCTTTTACGGACAACTCGTCCCTCCGGCCGTACCGGAGACATTCAGGT	2399
5427	GCGGTCCCGGCTTTTACGGACAACTCGTCCCTCCGGCCGTACCGGAGACATTCAGGT	5486
2400	GCGGCATCTACAGCCCTCTGTTAGCGGCAAGAGCACTAAGGTGCGGGTGCCTATGC	2459
5487	GCGGCATCTACAGCCCTCTGTTAGCGGCAAGAGCACTAAGGTGCGGGTGCCTATGC	5546
2460	AGCCCAAGGTTATAGGTGCTTCTCTGAAACCGCTCGCGCCACCCCTAGGTTTCGG	2519
5547	AGCCCAAGGTTATAGGTGCTTCTCTGAAACCGCTCGCGCCACCCCTAGGTTTCGG	5606
2520	GCGGTATATGCTAAGGCACATGTTATCGACCTTAACATCAGAACCGGGGTGAAGACCAT	2579
5607	GCGGTATATGCTAAGGCACATGTTATCGACCTTAACATCAGAACCGGGGTGAAGACCAT	5666
2580	CACCAAGGTTGCCCCCATCAGTACTCCACCTATGCGAAGTTCTTCCGCGAGGTGTTG	2639
5667	CACCAAGGTTGCCCCCATCAGTACTCCACCTATGCGAAGTTCTTCCGCGAGGTGTTG	5726
2640	CTCTGGGGCGCTATGATCATATAATGATGATGAGTGCCTCAACTGACTCGACAC	2699
5727	CTCTGGGGCGCTATGATCATATAATGATGATGAGTGCCTCAACTGACTCGACAC	5786
2700	TATCTGGGCATCGGCACAGTCTCTGGAACAGCGGAGCGGTGAGCGCGACTCGTCTG	2759
5787	TATCTGGGCATCGGCACAGTCTCTGGAACAGCGGAGCGGTGAGCGCGACTCGTCTG	5846
2760	GCTCGCCACCGCTACGCCCTCCGGGATCGGTACCGTGCACATCCAAACATCGAGAGGT	2819
5847	GCTCGCCACCGCTACGCCCTCCGGGATCGGTACCGTGCACATCCAAACATCGAGAGGT	5906
2820	GGCTGTCTCCAGCCTGGAGAAATCCCTTTTATGGCAAGCCATCCCATCGAGACCAT	2879
5907	GGCTGTCTCCAGCCTGGAGAAATCCCTTTTATGGCAAGCCATCCCATCGAGACCAT	5966
2880	CAAGGGGGGAGGCACCTCATTTTCTGCCATTTCCAAAGAGAAATGTATGATCGCCGC	2939
5967	CAAGGGGGGAGGCACCTCATTTTCTGCCATTTCCAAAGAGAAATGTATGATCGCCGC	6026
2940	GAAGCTGTCCGGCTCGGACTCAATGCTGTAGCATATATACCGGGGCTTGTATGATCGGT	2999
6027	GAAGCTGTCCGGCTCGGACTCAATGCTGTAGCATATATACCGGGGCTTGTATGATCGGT	6086
3000	CATACCAATAGCGGAGAGCGTCAATTTGCTAGCAACCGAGCGTCTTAATGCGGGCTTTAC	3059
6087	CATACCAATAGCGGAGAGCGTCAATTTGCTAGCAACCGAGCGTCTTAATGCGGGCTTTAC	6146
3060	CGGCGATTCGACTGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGC	3119
6147	CGGCGATTCGACTGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGC	6206
3120	CCTGGACCCGACCTTACACCATTCAGACGACGCGGTGCCCAAGACGCGGTGTCCGCTC	3179
6207	CCTGGACCCGACCTTACACCATTCAGACGACGCGGTGCCCAAGACGCGGTGTCCGCTC	6266

Qy	3180	GCACGGCGCAGGACGAGCACTGGTATAGCGGAGGATGGCATTTTACAGGTTTGTGATCTCCAGG	33239
Db	6267	GCAGCGCGCAGGACGAGCACTGGTATAGCGGAGGATGGGCATTTTACAGGTTTGTGATCTCCAGG	6326
Qy	3240	AGAA CGGCCCTCGGGCATGTTTCGATTCCTCGGTTCTGTGCGAGTGCATATGACCGGGCTG	32999
Db	6327	AGAA CGGCCCTCGGGCATGTTTCGATTCCTCGGTTCTGTGCGAGTGCATATGACCGGGCTG	6386
Qy	3300	TGCTTGGTACGAGCTACAGCGCGCGGAGACCTCAGTATAGGTTTGGGGCTTACCTAAACAC	3359
Db	6387	TGCTTGGTACGAGCTACAGCGCGCGGAGACCTCAGTATAGGTTTGGGGCTTACCTAAACAC	6446
Qy	3360	ACCAGGGTTGCCGCTCTGCACGACCATCTCGAGTTCTGGGAGAGCGTCTTTACAGGCCT	3419
Db	6447	ACCAGGGTTGCCGCTCTGCACGACCATCTCGAGTTCTGGGAGAGCGTCTTTACAGGCCT	6506
Qy	3420	CACCCACATAGACGCCCATTTCTGTGCCAGACTAAGCAGGACGACAACTTCCCTTA	3479
Db	6507	CACCCACATAGACGCCCATTTCTGTGCCAGACTAAGCAGGACGACAACTTCCCTTA	6566
Qy	3480	CCTGCTAGCATACCAAGGCTACGCTGTGCGCCAGGGCTCAGGCTCCACTCGTGGGA	3539
Db	6567	CCTGCTAGCATACCAAGGCTACGCTGTGCGCCAGGGCTCAGGCTCCACTCGTGGGA	6626
Qy	3540	CCAAATGTGGAAGTGTCTCATACGGCTAAAGCCTTACGCTCAGCGGCCAACGCCCTGCT	3599
Db	6627	CCAAATGTGGAAGTGTCTCATACGGCTAAGCCTTACGCTCAGCGGCCAACGCCCTGCT	6686
Qy	3600	GTATAGGCTGGAGCGGTTCAAAACGAGGTTTACTACCAACACCCCAATACCAATACAT	3659
Db	6687	GTATAGGCTGGAGCGGTTCAAAACGAGGTTTACTACCAACACCCCAATACCAATACAT	6746
Qy	3660	CATGCGCATGATCCTCGGCTGACCTGAGGTCGTCAAGACACCTGGGTGTGTAGCGG	3719
Db	6747	CATGCGCATGATCCTCGGCTGACCTGAGGTCGTCAAGACACCTGGGTGTGTAGCGG	6806
Qy	3720	AGTCCTAGCAGCTCTGGCCGCGTATTGCCCTGACAAACAGGACGCTGTCATTGTGGGAG	3779
Db	6807	AGTCCTAGCAGCTCTGGCCGCGTATTGCCCTGACAAACAGGACGCTGTCATTGTGGGAG	6866
Qy	3780	GATCATCTTGTCCGGAAGCGCGGCATCATTCCTCGACAGGAAGTCTTTACCGGAGTT	3839
Db	6867	GATCATCTTGTCCGGAAGCGCGGCATCATTCCTCGACAGGAAGTCTTTACCGGAGTT	6926
Qy	3840	CGATGAGATGGAAGAGTGCSCCTCACACCTCCCTTATCTCGACAGGGAATCGAGCTGC	3899
Db	6927	CGATGAGATGGAAGAGTGCSCCTCACACCTCCCTTATCTCGACAGGGAATCGAGCTGC	6986
Qy	3900	CGAACAAATCAAAACAGAAAGCAATCGGGTTGTGCAAAACAGACCAACAGAGCGGAGGC	3959
Db	6987	CGAACAAATCAAAACAGAAAGCAATCGGGTTGTGCAAAACAGACCAACAGAGCGGAGGC	7046
Qy	3960	TGCTGCTCCCGTGGTGGATCCAAGTGGCGACCTTCGGAAGCCTTCTGGGGAAGCATAT	4019
Db	7047	TGCTGCTCCCGTGGTGGATCCAAGTGGGGAAGCATTCGAAGCCTTCTGGGGAAGCATAT	7106
Qy	4020	GTGGAATTTTCATCAGCGGGATACAATATTTAGCAGGCTGTCCACTCTGCTGGCAACCC	4079
Db	7107	GTGGAATTTTCATCAGCGGGATACAATATTTAGCAGGCTGTCCACTCTGCTGGCAACCC	7166
Qy	4080	CGCGATAGCATCTGATGCAATTCACGCGCTTATCACCGCCCGCTCACACCCCAACA	4139
Db	7167	CGCGATAGCATCTGATGCAATTCACGCGCTTATCACCGCCCGCTCACACCCCAACA	7226
Qy	4140	TACCTTCTGTTTTAAATCTCTGGGGGATGGGTGGCGGCCCAACTTGTCTCTCCAGCGC	4199
Db	7227	TACCTTCTGTTTTAAATCTCTGGGGGATGGGTGGCGGCCCAACTTGTCTCTCCAGCGC	7286
Qy	4200	TGCTTCTGTCTTTCGTAGGCGCGGGATCGCTCGAGGGGCTGTGTGCACATAGGCTTGG	4259
Db	7287	TGCTTCTGTCTTTCGTAGGCGCGGGATCGCTCGAGGGGCTGTGTGCACATAGGCTTGG	7346

QY	4260	GAAGGTGCTTGTGGATATTTTGGCAGGTATATGGACAGGGGTGGCAGCGCGCTCGTGGC	4319
Db	7347	GAAGGTGCTTGTGGATATTTTGGCAGGTATATGGACAGGGGTGGCAGCGCGCTCGTGGC	7406
QY	4320	CTTTAAGGTCAATGAGCGGGAGATGCCCTCCACGAGGACCTGGCTAACCTTACTCCCTGC	4379
Db	7407	CTTTAAGGTCAATGAGCGGGAGGTGGCCCTCCACGAGGACCTGGTTAACTTACTCCCTGC	7466
QY	4380	TATCCTCTCCCCCTGGCGCCCTAGTTCGTCCGGGTCTGTGCGCAGCATCTGCGTCGGCA	4439
Db	7467	TATCCTCTCCCCCTGGCGCCCTAGTTCGTCCGGGTCTGTGCGCAGCATCTGCGTCGGCA	7526
QY	4440	CGTGGGCCACGAGGAGGGGCTGTGCATGGATGAACCGGTGATACGCTTTCGCTTCGCG	4499
Db	7527	CGTGGGCCACGAGGAGGGGCTGTGCATGGATGAACCGGTGATGAACCGGTTCGCTTCGCG	7586
QY	4500	GGTAACCAACGCTCCCCCGACGCACTATGTGCTGAGAGCGACGCTCGACGACGCTGTCAC	4559
Db	7587	GGTAACCAACGCTCCCCCGACGCACTATGTGCTGAGAGCGACGCTCGACGACGCTGTCAC	7646
QY	4560	TCAGATCCTCTCTAGTCTTACCATCACTCAGCTGCTCAAGAGGCTTCACCAAGTGAATCAA	4619
Db	7647	TCAGATCCTCTCTAGTCTTACCATCACTCAGCTGCTCAAGAGGCTTCACCAAGTGAATCAA	7706
QY	4620	CGAGACTGTGTCAGGCGCATGCTCCGGCTCGTGGCTAAGAGATGTTTGGATTTGGATATG	4679
Db	7707	CGAGACTGTGTCAGGCGCATGCTCCGGCTCGTGGCTAAGAGATGTTTGGATTTGGATATG	7766
QY	4680	CACGGTGTGACTCATTTCAAGACCTTGCTCCAGTCCAAGCTCCTGCGCGGATTCGCGG	4739
Db	7767	CACGGTGTGACTCATTTCAAGACCTTGCTCCAGTCCAAGCTCCTGCGCGGATTCGCGG	7826
QY	4740	AGTCCCTTCTTCTCATGTCAACGTGGGTACAAAGGAGTCTGCGCGGGCGAGCGCATCAT	4799
Db	7827	AGTCCCTTCTTCTCATGTCAACGTGGGTACAAAGGAGTCTGCGCGGGCGAGCGCATCAT	7886
QY	4800	GCAACACACCTGCCATGTGGAGACAGATCACCGGACATGTGAAAAAGTTTCCATGAG	4859
Db	7887	GCAACACACCTGCCATGTGGAGACAGATCACCGGACATGTGAAAAAGTTTCCATGAG	7946
QY	4860	GATCGTGGGCTTAGGACCTGTAGTAACAGTGGCATGGAACTTCCCATTAACGCGTAA	4919
Db	7947	GATCGTGGGCTTAGGACCTGTAGTAACAGTGGCATGGAACTTCCCATTAACGCGTAA	8006
QY	4920	CACCAACGGGCCCCGTGCAAGCCCTCCCGCGCGCCAAATTTCTTAGGGCGCTCTGCGCGGT	4979
Db	8007	CACCAACGGGCCCCGTGCAAGCCCTCCCGCGCGCCAAATTTCTTAGGGCGCTCTGCGCGGT	8066
QY	4980	GGCTGCTGAGGAGTACGTGGAGGTTACGGGGTGGGGATTTCCCACTACGTACAGGGCAT	5039
Db	8067	AGGTGCTGAGGAGTACGTGGAGGTTACGGGGTGGGGATTTCCCACTACGTACAGGGCAT	8126
QY	5040	GACCACTGACAAAGTAAAGTGGCCGCTGTCAGTTCGGGCCCCCGAAATTTCTTACAGAGT	5099
Db	8127	GACCACTGACAAAGTAAAGTGGCCGCTGTCAGTTCGGGCCCCCGAAATTTCTTACAGAGT	8186
QY	5100	GGATGGGGTGGCTTGCAAGGATACGCTCACGCTGTCAAAACCCCTCTTACGGGAGGAGGT	5159
Db	8187	GGATGGGGTGGCTTGCAAGGATACGCTCACGCTGTCAAAACCCCTCTTACGGGAGGAGGT	8246
QY	5160	CACATTTCTGCTGGGCTCAATCAATCTTGTTGGGTACAGTTCCTCATCGAGCCCGA	5219
Db	8247	CACATTTCTGCTGGGCTCAATCAATCTTGTTGGGTACAGTTCCTCATCGAGCCCGA	8306
QY	5220	ACCGGACGTAGCAGTCTCACATTTCCATGCTCACAGACCCCTCCACATTACGGCGGAGAC	5279
Db	8307	ACCGGATGTAGCAGTCTCACATTTCCATGCTCACAGACCCCTCCACATTACGGCGGAGAC	8366
QY	5280	GGCTAAGCTAGGCTGGCCAGGGGATCTCCCGCTTGTGGCCAGCTCATCAGCTAGCCA	5339
Db	8367	GGCTAAGCTAGGCTGGCCAGGGGATCTCCCGCTTGTGGCCAGCTCATCAGCTAGCCA	8426
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QY	7560	CAACTGGCGCAGTGAAGACCAAGCTCAAACTCACTCCAAATCCCGGCTGGCTCCCACTTGG	7619
Db	10647	CAACTGGCGCAGTGAAGACCAAGCTCAAACTCACTCCAAATCCCGGCTGGCTCCCACTTGG	10706
QY	7620	TTTATCCAGCTGGTTCGTTCTGGTTACAGCGGGGAGACATATATCACACGCTGTCTCG	7679
Db	10707	TTTATCCAGCTGGTTCGTTCTGGTTACAGCGGGGAGACATATATCACACGCTGTCTCG	10766
QY	7680	TGCCGACCCCGCTGGTTCAATGTGGTGCCTACTCTACTTCTCTAGGGGTAGCACTCA	7739
Db	10767	TGCCGACCCCGCTGGTTCAATGTGGTGCCTACTCTACTTCTCTAGGGGTAGCACTCA	10826
QY	7740	TCCTACTCCCCACCGATGAACGGGGAGCTAAACACATCCAGGCCAATAGGCCATCCTGTTT	7799
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QY	7800	TTTTCCCTTTTTTTTTTTCTTT	7859
Db	10887	TTTTCCCTTTTTTTTTTTCTTT	10946
QY	7860	TTTTTTCCTTTTTTTTTTCCTTTTCTTTCCCTTGGTGCCTCACTTAGCCCTAGTCACGG	7919
Db	10947	TTTTTTCCTTTTTTTTTTCCTTTTCTTTTGGTGGCTCCACTTAGCCCTAGTCACGG	11006
QY	7920	CTAGCTGTGAAGGTCCTGGAGCCGCTTCAGCTGCAGAGAGTGTGATCTGGCGCTCTCG	7979
Db	11007	CTAGCTGTGAAGGTCCTGGAGCCGCTTGACTGCAGAGAGTGTGATCTGGCGCTCTCG	11066
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Db	11067	CAGATCAAGT	11076

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RESULT 12
US-09-014-416-4
; Sequence 4, Application US/09014416
; Patent No. 6153421
; GENERAL INFORMATION:
; APPLICANT: Yanagi, Masayuki
; APPLICANT: Buhk, Jens
; APPLICANT: Emerson, Susanne U.
; APPLICANT: Purcell, Robert H.
; TITLE OF INVENTION: CLONED GENOMES OF INFECTIOUS HEPATITIS C VIRUSES AND
; TITLE OF INVENTION: USES THEREOF

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/ FILE REFERENCE: 20264276
/ CURRENT APPLICATION NUMBER: US/09/014.416
/ CURRENT FILING DATE: 1998-01-27
/ EARLIER APPLICATION NUMBER: US 60/053.062
/ EARLIER FILING DATE: 1997-07-18
/ NUMBER OF SEQ ID NOS: 65
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 4
/ LENGTH: 9595
/ TYPE: DNA
/ ORGANISM: Hepatitis C virus
/ US-09-014.416-4

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Query Match	66.5%;	Score 5312;	DB 3;	Length 9595;
Best Local Similarity	91.3%;	Pred. No. 0;		

	Matches 5650;	Conservative	0;	Mismatches	530;	Indels	10;	Gaps	1;
QY	1800	CATGGCGCCTATTACGGCCTACTCCCAACAGACGCGAGGCGTACTTGGCTGCATCATCAC							1859
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QY	1860	TAGCCTCACAGGCGGGACAGGAACACAGTCTGAGGGGAGGTCCAGGTGTCTCCACCGC							1919
Db	3476	TAGCCTCACAGGCGGGACAAGAACACAGTCTGAGGGGAGGTTCAAGTGGTTCTTACCGC							3535
QY	1920	AACACAATCTTTCTGGCGACCTGCGTCAATGCGGTGTGTGACACTGTCTATCATGGTGC							1979
Db	3536	AACACAATCTTTCTGGCGACCTGCGATCAACGCGGTGTCTGGACTGTCTACCATGGCGC							3595

QY	1980	CGGCTCAAGACCCCTTGCCGGCCCAAAAGGCGCCAAATCACCCCAAATGTACACCAATGTGGA	2039
DB	3596	TGGCTCGAAGACCCCTAGCCGGTCCAAAGGTCOAATCACCCAAATGTACACCAATGTAGA	3655
QY	2040	CCAGAGACTTCGTGGCTGGCAAGCGCCCCCGGGGGCGGTTCTTGTGACACCATGACACTG	2099
DB	3656	CGTGACCTCGTGGCTGGCAGGCGGCCCGCGGGCGCGCTCCATGACACCATGACACTG	3715
QY	2100	CGGCACTCGGACCTTTACTTTGGTTCAGAGGACATGCCGATGTCTATTCGGTGGCGCGCG	2159
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QY	2160	GGGCGACAGCAGGGGAGCCTACTCTCCCGCAGCGCCCGTCTCTACTTTGAAGGCTCTTC	2219
DB	3776	AGGCGACAGCAGGGGAACTTACTCTCCCGCAGGCCCGTCTCTACTCTGAAGAGCTCTCTC	3835
QY	2220	GGGCGGTCACATGCTCTCTGCCCTCGGGGCAAGCTGTGGGCATCTTTTGGGCTCCCGTGTG	2279
DB	3836	GGGTGGTCCATTTGCTTTGCCCTTCGGGGCACGTGTGGGCGTCTTCGGGCTCTCTGTGTG	3895
QY	2280	CACCCGAGGGGTTCGGAAGGCGGTGGACTTTGTACCGCTGAGTCTATGAAACCACTAT	2339
DB	3896	CACCGGGGGTTCGGAAGGCGGTGGACTTCTATACCGTTGAGTCTATGAAACTACCAT	3955
QY	2340	CGGTCGCCCGTCTTTCACGGACAACTCGTCCCTTCGGCGCTACCGAGACATTCACAGT	2399
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DB	4016	GGCACATCTGCAAGCTCTTACTGGCAGCGGCAAGAGCACCAAGTGCCTGGCTATGC	4075
QY	2460	AGCCCAAGGCTATAAGTGTCTGCTCTGAACCGTCCGTCGCGCCACCTTAGTTCGG	2519
DB	4076	AGCCCAAGGCTACAAGTGTCTGCTGAACCGTCCGTCGCGCCACCTTAGGCTTGG	4135
QY	2520	GGCGTATATCTTAAGGCACATGCTATCGACCTTAACATCAGAACCGGGGTAGGACCAT	2579
DB	4136	GGCGTATATCTCAAGGCACACGCTATCGACCTTAACATCAGAACTGGGGTAGGACCAT	4195
QY	2580	CACGACGGGTGCCCCATCACTGCTATCCACTATGSCAAAGTTCTTTCGCGACGGTGGTGTG	2639
DB	4196	TACCAAGGGCGGCTTACGCTATGCTATGCTTCCACTATGSCAAAGTTCTTTCGCGACGGTGGTGTG	4255
QY	2640	CTCTGGGGCGCTATGACATCATATATGCTATGAGTGCCACTCAACTGACTCGAACAC	2699
DB	4256	TTCTGGGGCGCTATGACATCATATATGCTATGAGTGCCACTCAACTGACTCGAACAC	4315
QY	2700	TATCTGGGCATCGGCACAGTCTCTGGAACCAAGCGAGACGGCTGGAGCGGCTGCTCGT	2759
DB	4316	CATCTTTGGGCATCGGCACAGTCTCTGGAACCAAGCGAGACGGCTGGAGCGGCTGCTCGT	4375
QY	2760	GCTCGCACGGCTACGCTTCGGGATTCGCTACCGTGCCCATCAAAACATCGAGGAGT	2819
DB	4376	GCTCGCACGGCTACGCTTCGGGATTCGCTACCGTGCCCATCAAAACATCGAGGAGT	4435
QY	2820	GGCTCTGTCCAGCACTGGAGAAATCCCTTTTATGGCAAGGCAATCCCATCGAGACCAT	2879
DB	4436	AGGCTGTCCAAATGAGAGATCCCCCTTATGGCAAGGCAATCCCATCGAGGCAAT	4495
QY	2880	CAAGGGGGGAGGCACCTCATTTTCTGCAATTCGAAGAGAAATGTGATGAGCTCGCGC	2939
DB	4496	CAAGGGGGGAGGCATCTCATTTTCTGCCATTCGAAGAGAAATGTGAGAGCTCGCGC	4555
QY	2940	GAACTGTCCGGCTTCGACCTCAATGCTGTAGCATATTCGCGGGCCCTTGATGATCCGT	2999
DB	4556	AAAGCTGACAGGCTTCGACCTGAACTGTAGCATATTCGCGGGCCCTTGATGATCCGT	4615
QY	3000	CATACCAACTAGCGAGACGCTCATTTGCTGTAGCAACGAGCTCTAATGACGGCTTTAC	3059
DB	4616	CATACCGCTATCGAGACGCTGTTGCTGGCAACAGCGCTCAATGACGGCTTTAC	4675

QY	3060	CGGCAATTTGACATCACTGATCGACTGCAATACATGATGTGTCAACCCAGACAGTFCGACTTCAG	3119	Db	5756	CACCTCTCTGTTTAAACATCTTGGGGGATGGGTGGTCCCACTCGCTCTCTCCACGCG	5815
Db	4676	CGGCGAATTTGACATCACTGATCGACTGCAATACATGATGTGTCAACCCAGACAGTFCGACTTCAG	4735	QY	4200	TGCTTTGCTTTTCTGATGGCGCGGCATCGCTGGAGACGGCTGTTGGCAGCAGTAGGCTTTGG	4259
QY	3120	CCTGGACCGGACCTTACCATTTAGAGACGACACCGTGGCCACAGACGGGTTTCAAGCTC	3179	Db	5816	TGCTCAGCTTTCTGCGGCGCGGCATCGCGGAGCGGCTGTTGGCAGCAGTAGGCTTTGG	5875
Db	4736	CTTGGATCCCACTTCACTTACCATTTAGAGACGACACCGTGGCCACAGACGGGTTTCAAGCTC	4795	QY	4260	GAAGGTCTTTGATATTTTGGCAGGTTATGGAGCAGGGGTGGCAGGCGCGCTCGTGGC	4319
QY	3180	GCAGGCGGAGGAGGAGTGTAGGGGAGGATGGGCAATTTACAGGTTTGTGACTCCAGG	3239	Db	5876	GAAGGTCTCTGTGACATCTTTGGCGGGCTATGGGCGAGGGGTAGCGGCGCATCTGTCG	5935
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QY	3240	AGAACGGGCGCTCGGCGATGTTTCGATTCCTCGGTTCTGTGCGAGTGTCTATGAGCGGGCTG	3299	Db	5936	CTTTAAGGTCAATAGCGCGGAGGTTGCCCTCCACCGAGGACCTGGTCAACTTACTCTCCCTGC	5995
Db	4856	AGAACGGGCGCTCGGCGATGTTTCGATTCCTCGGTTCTGTGCGAGTGTCTATGAGCGGGCTG	4915	QY	4380	TATCTCTCTCCCTGGCGGCTTGTGCTGGGGTCTGTGCGAGGCTGTGCGAGCATCTGCGTCGGCA	4439
QY	3300	TGCTTGTAGAGCTCAGCGCGCGGAGACCTCAGTTAGTTGCGGGCTTACCTAAACAC	3359	Db	5996	CATCTCTCTCTGGTGCCTGGTCTGGGGTCTGTGCGAGGCTGTGCGAGCATCTGCGTCGGCA	6055
Db	4916	TGCTTGTATGAGCTCAGCGCGCGCTGAGACCTCGGTTAGTTGCGGGCTTACCTAAATAC	4975	QY	4440	CGTGGGCGGAGGGAGGGGCTGTGCACTGGATGAACCGGCTGTAGCGTTGCTTCGCG	4499
QY	3360	ACCAGGTTGCGCGTCTGCCAGGACCATCTGGAGTTCTGGGAGAGCGTCTTTACAGGCT	3419	Db	6056	CGTGGGCGGAGGAGGGGGCTGTGCACTGGATGAACCGGCTGTAGCGTTGCTTCGCG	6115
Db	4976	ACCAGGTTGCGCGTCTGCCAGGACCATCTGGAGTTCTGGGAGAGCGTCTTTACAGGCT	5035	QY	4500	GGGTAAACACAGTCTCCCGACGCACTATGTGCTGAGAGCGAGCTGAGACAGCTGTCTAC	4559
QY	3420	CACCCACATAGACGCCCATTTCTGTGCCAGACTAAGCGAGGAGGAGCAACTTCCCTTA	3479	Db	6116	GGGTAAACACAGTCTCCCGACGCACTATGTGCTGAGAGCGAGCTGAGACAGCTGTCTAC	6175
Db	5036	CACCCACATAGATGCCCATTTCTGTGCCAGACTAAGCGAGGAGGAGCAACTTCCCTTA	5095	QY	4560	TCAGATCTCTCTAGTCTTACCATCACTCAGCTGTCTGAAGGGCTTACCAGTGGATCAA	4619
QY	3480	CTGTGTAGATCAGAGGTACCGTGTGCGCAGGGCTCAGGCTCCACCTCCATCTGTGGGA	3539	Db	6176	TCAGATCTCTCTAGCTTACCATCACTCAGCTGTCTGAAGGGCTTACCAGTGGATCAA	6235
Db	5096	CTGTGTAGATCAGAGGTACCGTGTGCGCAGGGCTCAGGCTCCACCTCCATCTGTGGGA	5155	QY	4620	CGAGCACTGCTCCACCGCATGCTCCGGCTCGTGGCTTAAGAGATGTTTGGGATTTGATATG	4679
QY	3540	CAAAATGTGGAATGCTCATACGGCTAAAGCTCAGCTGCGAGGGCCAAACGCCCTGCT	3599	Db	6236	TCAGGACTGCTCTAGCGCATGCTCCGGCTCGTGGCTAAGGGATGTTTGGGATTTGATATG	6295
Db	5156	CAAAATGTGGAATGCTCATACGGCTAAAGCTCAGCTGCGAGGGCCAAACGCCCTGCT	5215	QY	4680	CACGGTGTGACTGATTTCAAGACCTGCTCAGTCCAGTCCAGTCTTCCCGCGATTCGCGG	4739
QY	3600	GTATAGGCTGGAGCGGTTTCAAAACGAGTTACTACACACACCCCATACCAATACAT	3659	Db	6296	CACGGTGTGACTGATTTCAAGACCTGCTCAGTCCAGTCCAGTCTTCCCGCGATTCGCGG	6355
Db	5216	GTATAGGCTAGGAGCGGTTTCAAAATGAGTCTCCTCACACACCCCATACCAATACAT	5275	QY	4740	AGTCCCTTCTTCTCATGCTCAAGTGGGTACAGGGAGTCTGGCGGGCGAGCGGCATCAT	4799
QY	3660	CATGGATGATGCTGGCTGACTGAGGTCTGACAGGCTGCTGACAGCACTGCTGGTAGGCGG	3719	Db	6356	AGTCCCTTCTTCTCATGCTCAAGTGGGTACAGGGAGTCTGGCGGGCGAGCGGCATCAT	6415
Db	5276	CATGGATGATGCTGGCTGACTGAGGTCTGCTGACGACCTGAGTCTGCTGGTAGGCGG	5335	QY	4800	GCAAAACCACTGCGCCATGTGGAGCAGATCACCGGACATGTGAAAAAGTTTCCATGAG	4859
QY	3720	AGTCTAGCAGCTCTGCGCGCGTATTGCTCTGACAAACAGGAGCGTGTCTATTTGGGCGAG	3779	Db	6416	GCAAAACCACTGCGCCATGTGGAGCAGATCACCGGACATGTGAAAAAGTTTCCATGAG	6475
Db	5336	AGTCTTGCAGCTTTGCGCGCATACTGCTGACGACAGGCACTGCTGATTTGGGCGAG	5395	QY	4860	GATCGTGGGCGCTTAGAACCTGTAGTAAACAGTGGCATGGAACATTTCCCATTAACCGTA	4919
QY	3780	GATCATCTTGTCCGGAAGCGCGCCATCATTTCCGACAGGGAAGTCTTTACCGGAGTT	3839	Db	6476	GATCGTGGGCGCTTAGAACCTGTAGTAAACAGTGGCATGGAACATTTCCCATTAACCGTA	6535
Db	5396	GATCATCTTGTCCGGAAGCGCAGTGTGCTTCCGACAGGGAAGTCTTACCAAGAGTT	5455	QY	4920	CACACGCGCGCTTACGACCTTCCCGCGCGCCCACTATTCCAGGCGGCTATGCGGGT	4979
QY	3840	CGATGAGATGGAAGTGGCTTCAACCTTCCCTTACATCGAAACAGGGAATGAGCTTCG	3899	Db	6536	CACACGCGGACCTTACGACCTTCCCGCGCGCCCACTATTCCAGGCGGCTATGCGGGT	6595
Db	5456	CGATGAGATGGAAGTGGCTTCAACCTTCCCTTACATCGAAACAGGGAATGAGCTTCG	5515	QY	4980	GGCTGTGTGAGAGTACGTGGAGGTTACGCGGGTGGGGGATTTCCATCTAGTACGGGCAT	5039
QY	3900	CGAAACAAATCAACAGAGGCAATCGGGTTGCTGCAAAACGCAACGCAAGCAAGCGGAGC	3959	Db	6596	GGCTGTGTGAGAGTACGTGGAGGTTACGCGGGTGGGGGATTTCCATCTAGTACGGGCAT	6655
Db	5516	CGAGCAATTCAGCAAAAGGCGTGGGTTGTTGCAAAACGCGCCACCAAGCAAGCGGAGC	5575	QY	5040	GACCACTGACAAAGTAAAGTCCCGTCAAGTTCAGGTTCCGCGCCCGCAATTTCTTACAGAGT	5099
QY	3960	TGCTGTCCCGTGGTGAATCCAAGTGGCGGACCTCGAGGCTTCTGGGCGAGCATAT	4019	Db	6656	GACCACTGACAAAGTAAAGTCCCGTCAAGTTCAGGTTCCGCGCCCGCAATTTCTTACAGAGT	6715
Db	5576	TGCTGTCCCGTGGTGAATCCAAGTGGCGGACCTCGAGGCTTCTGGGCGAGCATAT	5635	QY	5100	GGATGGGCTCGGTTGACAGGTAAGTCCAGGTTGCAAAACCTTCTTCTACGGGAGGAGT	5159
QY	4020	GTGGAATTTTCATAGCGGGATACAATATTTAGCAGGCTTGTCTCACTGCTGCTGCAACCC	4079	Db	6716	GGATGGGCTCGGTTGACAGGTAAGTCCAGGTTGCAAAACCTTCTTCTACGGGAGGAGT	6775
Db	5636	GTGGAATTTTCATAGCGGGATACAATATTTAGCAGGCTTGTCTCACTGCTGCTGCAACCC	5695	QY	5160	CACATTTCTGCTCGGCTCAATCAATACCTGTTGGTTCAGCTCCATTCGAGCGGAGCCGA	5219
QY	4080	CGCGATAGCATCACTGATGGAATTCAGAGCTTATCACAGCGCGCTTACCAACCGAC	4139	Db	6776	CACGTTCCAGTTCGGGCTCAACCAATATCTTGGTTCGGGTCGAGCTCCCATCGAGCCCGA	6835
Db	5696	CGCGATAGCATCACTGATGGAATTCAGAGCTTATCACAGCGCGCTTACCAACCGAC	5755	QY	5220	ACCGGAGTAGCAGTGTCTCTTCCATGCTCACCGACCCCTTCCACATTTACGGCGGAGAC	5279
QY	4140	TACCTCTCTGTTTAACTCTTGGGGGATGGGTGGCGCGCCCAACTTGTCTCTCCAGCGC	4199				

Db	6836	ACCGACGTAACAGTGTCTTACTTCCATGCTCACCGATCCCTCCACATTACAGCAGAC	6895
QY	5280	GGCTAAGCGTAGGTGGCCAGGGATCTCCCTCCCTCTTGGCCAGCTCATCAGCTAGCCA	5339
Db	6896	GGCTAAGCGTAGGTGGCTAGAGGTCTCCCTCCCTCTTAGCCAGCTCATCAGCTAGCCA	6955
QY	5340	GCTGTCTGCGCTTCTTTGAAGGCAACATGCACTACCCGTCATGACTCCCGGAGCGTGA	5399
Db	6956	GTTGTCTGCGCTTCTTTGAAGGCGACATGCACTACCCATGACTCCCGGAGCGTGA	7015
QY	5400	CCTCATCGAGGCGCAACCTCTCTGTGGCGGAGAGATGGCGGGGAAATCACTACCCCGGTGGA	5459
Db	7016	CCTCATCGAGGCGCAACCTCTCTGTGGCGGAGAGATGGCGGGGAAATCACTACCCCGGTGGA	7075
QY	5460	GTCAAGAAATAGGTAGTAATTTTGGACTCTTTGAGCGGCTCCAGCGGAGAGGATGA	5519
Db	7076	GTCAAGAAATAGGTAGTAATTTTGGACTCTTTGAGCGGCTCCAGCGGAGAGGATGA	7135
QY	5520	GAGGGAAGTATCCGTTCCGGCGGAGATCTCTCGGAGGTCCAGGAAATTCCTTCGAGCGAT	5579
Db	7136	GAGGGAAGTATCCGTTCCGGCGGAGATCTCTCGGAAATTCAGGAAGTTCCTTCAGCGTT	7195
QY	5580	GCCCATATGGCAGCCCGGATTAACAACCTCCACTGTTAGAGTCTCTGGAAGACCCGGA	5639
Db	7196	GCCCATATGGCAGCCCGGACTACAATCTCTCCACTGCTAGAGTCTCTGGAAGACCCGGA	7255
QY	5640	CTAGCTCCCTCCAGTGTACACGGGTGTCATTGCGGCTGCCAAGGCCCTCCGATACC	5699
Db	7256	CTAGCTCCCTCCAGTGTACACGGATGCCANTGCCACCTACCAGGCTCTCTCAATACC	7315
QY	5700	ACCTCCACGGGAAGAGGACGGTTGTCCTGCAGAAATCTACCGTCTCTTCTGCTTTGGC	5759
Db	7316	ACCTCCACGGGAAGAGGACGGTTGTCCTGCAGAAATCCAAATGTCTCTGCTTTGGC	7375
QY	5760	GGAGCTCGCCACAAAGACCTTCGCACTCGGAATCGTGGCGCTGCACAGCGGCACGG	5819
Db	7376	GGAGCTCGCCACTAAGACCTTCGCTAGCTCCGATCTCGGCTGCTGATAGCGGCACGG	7435
QY	5820	AACGGCTCTCTTACACGACCTCCGACGCGGAGCGGAGTCCGATCTCAGACCGGCTCTG	5879
Db	7436	GACCGCTCTCTTACCTGCGCTCCGACGCGGAGCGGAGTCCGATCTCAGACCGGCTCTG	7495
QY	5880	CTCCTCCATGCCCTTGAAGGGAGCGCGGGGATCCCGATCTCAGACCGGCTCTG	5939
Db	7496	CTCCTCCATGCCCTTGAAGGGAGCGCGGGGACCCGATCTCAGACCGGCTCTG	7555
QY	5940	GTCTACCGTAAGCAGAGGCTAGTAGGACGTCTGCTGCTGCTGCTGCTGCTGCTGCTG	5999
Db	7556	GTCTACCGTAGTAGGAGGCTAGTAGGATGTCTGCTGCTGCTGCTGCTGCTGCTGCTG	7615
QY	6000	GACAGCGCCTGATCAGCGCATGCGCTGCGGAGGAAACCAAGCTGCCATCAATGCACT	6059
Db	7616	GACAGCGCCTGATCAGCGCATGCGCTGCGGAGGAAAGTAAGCTGCCATCAATGCACT	7675
QY	6060	GAGCAACTCTTTGCTCCGTACCAACAATCTGTTGCTATGTTACAACTCTCGACGCGCAAG	6119
Db	7676	GAGCAACTCTTTGCTCCGTACCAACAATCTGTTGCTATGTTACAACTCTCGACGCGCAAG	7735
QY	6120	CTTGCGGAGAGAGGCTACCTTTGACAGACTGCGAGGCTCTGGAAGCACTACCGGGA	6179
Db	7736	CTTGCGGAGAGAGGCTACCTTTGACAGACTGCGAGGCTCTGGAAGCACTACCGGGA	7795
QY	6180	CGTGCTCAAGGAGATGAAGCGGCTCCAGTTAAGGCTAAAGCTCTATCTCCGTGA	6239
Db	7796	CGTACTCAGGAGATGAAGCGGAGGCTCCAGTTAAGGCTAAAGCTCTATCTATAGA	7855
QY	6240	GGAAGCCTGTAGCTGACGCCGCCCACTTCGGCCAGATCTAAATTTGGCTATGGGGCAAA	6299
Db	7856	GGAAGCCTGTAGCTGACGCCGCCCACTTCGGCCAAATCCAAATTTGGCTATGGGGCAAA	7915
QY	6300	GGACGCTCCGGAACCTATCCAGCAGGCGGTTAACCACTCCGCTCCGTTGGAAGACTT	6359
Db	7916	GGACGCTCCGGAACCTATCCAGCAGGCGGTTAAACCACTCCGCTCCGTTGGAAGACTT	7975
QY	6360	GCTGGAAGACACTGAGACACCAATTGACACCACTCATGGCAAAATAGAGTTTCTG	6419
Db	7976	GCTGGAAGACACTGAAACCAATTTGACACCACTCATGGCAAAATAGAGTTTCTG	8035
QY	6420	CGTCCAAACAGAGAGGGGGCCGACGCTGCGCTTATCGTATTTCCAGATTTGGG	6479
Db	8036	CGTCCAAACAGAGAGGGGGCCGACGCTGCGCTTATCGTATTTCCAGAGACTGGG	8095
QY	6480	GTTTCGTGTGTCGAGAAATGGCCCTTTAGATGTGTCTCCACCTCCCTCAGGCCGT	6539
Db	8096	AGTTTCGTGTGTCGAGAAATGGCCCTTTAGATGTGTCTCCACCTCCCTCAGGCCGT	8155
QY	6540	GATGGGCTCTTCATACGGAATCCAAATCTCTCTGGAAGCGGCTCGAGTTCTCGGTGAA	6599
Db	8156	GATGGGCTCTTCATACGGAATTTCAATCTCCCCCAAGCAGCGGCTCGAGTTCTCGGTGAA	8215
QY	6600	TGCTGGAAGCGGAGAAATGCCCTATGGGTTTGGATATGACACCCGCTCTTTTGACTC	6659
Db	8216	TACCTGGAATCAAAGAAATGCCCTATGGGTTTGGATATGACACCCGCTCTTTTGACTC	8275
QY	6660	AACGGTCACTGAGAAATGACATCTCGTGTGAGGAGTCAATCTACCAATGTTGAGCTTGGC	6719
Db	8276	AACGGTCACTGAGAGTGAATCTCGTGTGAGGAGTCAATTTACCAATGTTGAGCTTGGC	8335
QY	6720	CCCCGAAGCAGACAGGCCATAAGGTCGCTCACAGAGCGGCTTTACATCGGGGCGCCCT	6779
Db	8336	CCCCGAAGCAGACAGGCCATAAGGTCGCTCACAGAGCGGCTTTACATCGGGGCGCCCT	8395
QY	6780	GACTAATCTAAAGGCGAGACTCGGCTATCGGCTGCGGCGGAGCGGCTGACTGAC	6839
Db	8396	GACTAATCTAAAGGCGAGAACTCGGCTATCGGCTGCGGCGGAGCGGCTGACTGAC	8455
QY	6840	GACGAGTGGGTAAATACCTCTCATGTTACTTTGAAGCGCGCTGCGGCGGAGCTG	6899
Db	8456	GACTAGTGGGTAAATACCTCTCATGTTACTTTGAAGCGGAGCTGCGGCGGAGCTG	8515
QY	5900	GAGGCTCCAGGACTGACGATGCTGCTGATGCGGAGAGCGCTTGTGCTTATCTGTGAAAG	6959
Db	8516	AAAGCTCCAGGACTGACGATGCTGCTGATGCGGAGAGCGCTTGTGCTTATCTGTGAAAG	8575
QY	6960	CGCGGAGCCCAAGAGAGCGAGGAGCGCTTACGGGCTTACCGAGGCTATGACTAGATA	7019
Db	8576	CGCGGAGCCCAAGAGAGAGCGAGGAGCGCTTACGGGCTTACCGAGGCTATGACTAGATA	8635
QY	7020	CTTGTGCCCCCTTGGGAGCCCGCCAAACAGAAATACGACTTGGAGTTGATAACATCATG	7079
Db	8636	TTCCGCCCCCTTGGGAGCGCGGATCGCCCCAAACAGAAATACGACTTGGAGTTGATAACATCATG	8695
QY	7080	CTCCTCAATGTCTAGTCCGCGACGATGCTGCGCAAAAGGGTGTACTCTCACCCTG	7139
Db	8696	TTCTCTCAATGTCTAGTCCGCGACGATGCTGCGCAAAAGGGTGTACTCTCACCCTG	8755
QY	7140	TGACCCCAACCCCTTGGCGGGCTGCGTGGGAGAGCTAGACACACTCCAGTCAA	7199
Db	8756	TGACCCCAACCCCTTGGCGGGCTGCGTGGGAGAGAGCTAGACACACTCCAGTCAA	8815
QY	7200	TTCTGCGCTAGGCAACATCATCATGTATGCGGCCACTTTGTGGGCAAGGATGATCTGAT	7259
Db	8816	CTCTGGCTTAGGCAATATCATCATGTATGCGGCCACTTATGGGCAAGGATGATCTGAT	8875
QY	7260	GACTCATTTTCTTCTCATCTTCTAGCTCAGGAAACAACTTGAAAGACCCCTAGATTGTCA	7319
Db	8876	GACTCATTTTCTTCTCATCTTCTAGCTCAGGAAACAACTTGAAAGACCCCTAGATTGTCA	8935
QY	7320	GATCTACGGGCGCTGTACTCCATTTGAGCACTTGAACCTTACCTCAGATCATTTCAAGCT	7379
Db	8936	GATCTACGGGCGCTGTACTCCATTTGAGCACTTGAACCTTACCTCAGATCATTTCAAGCT	8995
QY	7380	CCATGGCCTTAGCGATTTTCACTCCATAGTTACTCTCCAGGTGAGATCAATAGGTTGGC	7439
Db	8996	CCATGGCCTTAGCGATTTTCACTCCATAGTTACTCTCCAGGTGAGATCAATAGGTTGGC	9055

QY	7440	TTTCATGCTCCAGAAACTTGGGGTACCGCCCTTTCGAGTCTCGAGACATCGGSCCAGAAG	7499
Db	9056	TTTCATGCTCCAGAAACTTGGGGTACCAACCTTGCACCTCGAGACATCGGSCCAGAAG	9115
QY	7500	TGTCGCGCTAGGCTACTGTCCAGGGGGAGGGGTGCACCTTGTGGCAAGTACTCCTTT	7559
Db	9116	TGTCGCGCTTAAGCTACTGTCCAGGGGGAGGGCGCCACTTGTGGCAGATACCTCCTTT	9175
QY	7560	CAACTGGGAGTAAGGACCAAGCTCAAACTCACTCCCAATCCCGGCTGCGTCCAGTTGGA	7619
Db	9176	TAACTGGGCGAGTAAGGACCAAGCTTAAACTCACTCCCAATCCCGCGCGCTCCAGCTGGA	9235
QY	7620	TTTATCTCAGCTGTTTCGTTCTGCTGTTACAGCGGGGAGACATATACAGCCTGTCTCG	7679
Db	9236	CTTTGCTGCTGTTTCGTCGCTGTTACAGCGGGGAGACATATATACAGCCTGTCTCG	9295
QY	7680	TGCCGACACCGCTGTTTCATGTTGTCCTACTTTCTGTAGGGGTAGGCATCTA	7739
Db	9296	TGCCGACACCGCTGTTTCGTTGTCCTACTTTCTGTAGGGGTAGGCATTTA	9355
QY	7740	TCTACTCCCCAAACCGATGAACGGGGAGCTAAACACTCCAGGCCAATAGGCCATCCTGTTT	7799
Db	9356	CCTGCTCCCCAAACCGATGAACGGGGAGCTAACCACTCCAGGCCCTTAAGCC-----	9405
QY	7800	TTTTTCCCTTTTTTTTTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCTCCTTT	7859
Db	9406	ATTTCCTGTTCTTTCTTTCTCT	9465
QY	7860	TTTTTTCCTCTTTTTTTTCTTTCTTTCTTTTGGTGCTCCACTTAGCCCTAGTACGG	7919
Db	9466	TCTTTTTTTCTTTCTTTTTCCTTCTTTAATGTGGCTCCATCTTAGCCCTAGTACGG	9525
QY	7920	CTAGCTGTGAAGGTCCGTGAGCCGCTTGACTGCGAGAGGTGCTGTACTTGGCCTCTCTG	7979
Db	9526	CTAGCTGTGAAGGTCCGTGAGCCGCTAGCTGCGAGAGGTGCTGTACTTGGCCTCTCTG	9585
QY	7980	CAGATCAAGT	7989
Db	9586	CAGATCATGT	9595

Best Local Similarity	91.8%	Pred. No. 0;	Mismatches	495;	Indels	0;	Gaps	0;
Matches	5515;	Conservative						
QY	1800	CATGGCGCCTATTACGGCCTACTCCCAACAGACGCGAGGCGCTACTTGGCTGCATCATCAC	1859					
Db	1908	CCTCGCGCCCATCACGGCCTACTCCCAACAGACGCGGGGCGCTACTTGGTTGCATCATCAC	1967					
QY	1860	TAGCCTTCACAGGCCGGGACAGGAACCAAGGTCGAGGGGGAGGTCACAGGTGGTCTCCACCCG	1919					
Db	1968	TAGCCTTCACAGGCCGGGACAGGAACCAAGGTCGAGGGAGAGGTTACAGTGGTGTTCACCCG	2027					
QY	1920	AACACAATCTTCTCGCGACCTGCGTCAATGCGCTGTGTGGACTGTCTATCATCGTGC	1979					
Db	2028	AACACAATCTTCTCGCGACCTGCGTCAAGCGCTGTGTGGACCGTTTACCATGCTGC	2087					
QY	1980	CGGCTCAAAGACCCCTTCGCGGCCCAAGGGCCCAATCACCCAAATGTACACCAATGTGA	2039					
Db	2088	TGGCTCAAAGACCTTAGCGCGCCAAAGGGGCCAATCACCCAGATGTACACTAATGTGA	2147					
QY	2040	CGAGGACCTCGTCGGCTGGCAAGCGCCCCCGGGCGCGTTCCTTCACACCAATGCACCTG	2099					
Db	2148	CGAGGACCTCGTCGGCTGGCCCAAGCCCCCGGGGGCGGTTCCTTCACACCAATGCACCTG	2207					
QY	2100	CGGCAGCTCGGACCTTTACTTTGTTCACGAGGCAATGCGGATGTCAATTCGGTGGCGCGG	2159					
Db	2208	TGGCAGCTCAGACCTTTACTTTGTTCACGAGACATGCTGACGTCAATTCGGTGGCGCGG	2267					
QY	2160	GGGCGACAGCAGGGGAGCGCTACTCTCCCCCAGCGCCCGTCTCCCTACTTTGAAGGCTCTTC	2219					
Db	2268	GGGCGACAGTAGGGGGAGCGCTCTCTCCCCCAGCGCTCTCTCTACTTTGAAGGCTCTTC	2327					
QY	2220	GGGCGGCTCCATGCTCTGCGCCCTCGGGGCGACGCTGGGGGCACTTTTCGGGCTGCGGTG	2279					

Db 2328 GGGTGTCCAGTCTCTGCCCCCTTGGGACGCTGTGGCACTCTTCGGGCTGCCGTATG 2387
QY 2280 CACCCGAGGGTTGCGAAGCGGTGACATTTGTATCCCGTGCAGTCTATGGAACCACTAT 2339
Db 2388 CACCCGGGGGTTGCGAAGCGGTGACATTTGTGCCCCGTAGAGTCCATGGAACACTAT 2447
QY 2340 GGGGTCCCCGGTCTTCCAGCAACCTCGTCCCTCCGGCCGTACCGACAGATTCAGGT 2399
Db 2448 GCGGTCTCCGGTCTTACCGCACTATCCCTCCCGCCCGGTACCGAGTCAITTCAGT 2507
QY 2400 GGGCCATCTACAGCCCTTCTGAGGCGCAAGAGCACTAAGTCCCGCTGCGTATGC 2459
Db 2508 GGGCCACCTTACAGCTCCCACTGGCAGCGCAAGAGTACTAAGTCCCGCTGCAATGC 2567
QY 2460 AGCCCAAGGGTATAGGTCTTCTGCTGACCCGCTCGTCCCGCCGACCTAGGTTTCGG 2519
Db 2568 AGCCCAAGGGTACAAGGTCTCGTCTCAATCCGTCGCTGCGCTACCTTAGGTTTGG 2627
QY 2520 GGGGTATATGTCTAAGGCACATGGTATCGACCTTAACATCAGAACCGGGTAAGACCAT 2579
Db 2628 GGGGTATATGTCTAAGGCACATGGTATCGACCTTAACATCAGAACCGGGTAAGACCAT 2687
QY 2580 CACACGGGTGCCCTTCACTACTCCACCTATGGCAAGTTTCTTGGCCGCGTGGTTG 2639
Db 2688 TACCACAGCGCCCCCGTCACTACTCTACCTATGGCAAGTTTCTTGGCCGCGTGGTTG 2747
QY 2640 CTCTGGGGCGCTATGACATCATATATGATGAGTGCACCTCAATGACTCGACAC 2699
Db 2748 CTCTGGGGCGCTTATGACATCATATATGATGAGTGCACCTCAATGACTCGACAC 2807
QY 2700 TATCTTGGGCATCGGCACAGTCTTGGACCAAGCGGAGACGGCTGGAGCGGACTCGTGT 2759
Db 2808 AATCTTGGGCATCGGCACAGTCTTGGACCAAGCGGAGACGGCTGGAGCGGCTTGTGT 2867
QY 2760 GCTCGCCACCGCTAGCGCTCCGGATCGGTACCGTGCACATCCAAACATCGAGGAGGT 2819
Db 2868 GCTCGCCACCGCTAGCGCTCCGGATCGGTACCGTGCACATCCAAACATCGAGGAGGT 2927
QY 2820 GGTCTGTCCAGACTCGGGAATCCCTTTTATGGCAAGCCATCCCATCGAGACCAT 2879
Db 2928 GGGCTGTCTAATCTGGAGAGTCCCTTCTATGGCAAGCCATCCCATTTGAAGCCAT 2987
QY 2880 CAAAGGGGGGAGGACCTCTATTTCTGCTCATTTCCAAAGAAATGTGATGAGCTCGCGC 2939
Db 2988 CAGGGGGGAGGACATCTATTTCTGTCAITCCAAAGAAATGTGATGAGCTCGCGC 3047
QY 2940 GAAGCTGTCCGGCTCGGACTCAATGTGTAGCATATTAACGGGGCTTGTATGTATCGT 2999
Db 3048 AAAGCTGTCCAGGCTCGGAATCAACGCTGTGGCGTATTAACGGGGCTCGATGTGTCCGT 3107
QY 3000 CATACCAACTAGCGGAGACGTCTATGTCGTAGCAACGAGCTCTAATGAGGGCTTTAC 3059
Db 3108 CATACCAACTATCGAGACGCTGTGTGTCGTGCAACGAGCTCTGATGAGGGCTATAC 3167
QY 3060 CGCGATTTTCGACTGATGATGCAATATGATGTGTCACCGAGACGAGCTGACATTCAG 3119
Db 3168 GGGCGCATTTGACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3227
QY 3120 CTTGGACCCGACTTACCATTTGAGAGCAGACCGTGGCCCAAGACGCGGTGTCAAGCTC 3179
Db 3228 CTTGGATCCCACTTACCATTTGAGAGCAGACCGTGGCCCAAGACGCGGTGTCAAGCTC 3287
QY 3180 GCAAGCGCGGAGGAGGAGTCTGAGGAGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGG 3239
Db 3288 GCAAGCGCGGAGGAGGAGTCTGAGGAGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGG 3347
QY 3240 AGAACCGCCCTCGGGCATGTTTCAATCTCTCGGTCTGTGAGTGTGATGATGATGATGATG 3299
Db 3348 AGAACCGCCCTCGGGCATGTTTCAATCTCTCGGTCTGTGAGTGTGATGATGATGATGATG 3407
QY 3300 TGTCTGGTACGAGCTCAGCGCCCGCAGACCTCAGTTAGGTGTGCGGGCTTACCTAAACAC 3359

Db 3408 TGGTTGGTACGAGCTCAOCCCCGCGGAGACCTCGTGTAGGTTCGGGCGCTACCTGAACAC 3467
QY 3360 ACCAGGGTTGCCCGTCTGCGAGGACCATCTGAGGATTCGGGAGAGCTCTTTACAGGCCCT 3419
Db 3468 ACCAGGGTTGCCCGTTCGGAGACCATCTGAGGATTCGGGAGAGTCTTTACAGGCCCT 3527
QY 3420 CACCCATAGATGACACTTCTTGTCCAGACTAAGCAGGAGGAGACAACTTCCCTTA 3479
Db 3528 CACCCATAGATGACACTTCTTGTCCAGACTAAGCAGGAGGAGGAGCACTTCCCTTA 3587
QY 3480 CTTGTAGCATACAGGCTACGTTGTGCGCAGGCTCAGGCTCAGCTTCCATCTGTTGGGA 3539
Db 3588 CTTGTAGCATACAGGCTACGTTGTGCGCAGGCTCAGGCTCAGGCTCAGCTTCCATCATGGA 3647
QY 3540 CCAATGTGGAAGTCTCTCATCGGCTAAAGCTACGCTGACGCGGCGCAACGCCCTGCT 3599
Db 3648 TCAATGTGGAAGTCTCTCATCGGCTAAAGCTACGCTGACGCGGCGCAACGCCCTGCT 3707
QY 3600 GTATAGGCTGGAGCCGTTCAAAACAGGTTACTACACACACACCCCATAAACAAATACAT 3659
Db 3708 GTACAGGCTGGAGCCGTCAGATGAGGTACCCCTCACCCACCCCATAAACAAATACAT 3767
QY 3660 CATGSCATGCACTGCGCTGACCTGAGGTGTCAGAGGCTGTCAGAGGACCTGGGTGCTGAGCGG 3719
Db 3768 CATGSCATGCACTGCGCTGACCTGAGGTGTCAGAGGCTGTCAGAGGACCTGGGTGCTGAGCGG 3827
QY 3720 AGTCTTAGCAGCTCTGCGCGGTATTTGCTGACAAACAGGAGTGTGCTGAGGAGTGTGTTGGGAG 3779
Db 3828 AGTCTTAGCAGCTCTGCGCGGTATTTGCTGACAAACAGGAGTGTGCTGAGGAGTGTGTTGGTAG 3887
QY 3780 GATCATCTTGTCCGAAAGCGCGGCATCATTTCCGACAGGGAAGTCTTTTACCGGAGTT 3839
Db 3888 GATCATCTTGTCCGAAAGCGCGGCATCATTTCCGACAGGGAAGTCTTTTACCGGAGTT 3947
QY 3840 CGATGAGTGAAGAGTGGCTCAGCTTCCCTTATCATCGAAAGGGAATGCGAGTGC 3899
Db 3948 CGATGAAATGGAAGTGGCTCAGCTTCCCTTATCATCGAGCAGGGAATGCGAGTGC 4007
QY 3900 CGAACTTCAAAAGAGGCAATCGGGTGTCTGCAAAACAGCAGCAGGAGGAGGAGG 3959
Db 4008 CGAGCAATCAAGCAGAAAGGCTCGGGTGTCTGCAAAACAGCAGCAGGAGGAGG 4067
QY 3960 TGTCTTCCGCTGTGGAATCCAAAGTGGCGACCTCTGAAAGCTTCTGGGCGAAGCATAT 4019
Db 4068 TGTCTTCCGCTGTGGAATCCAAAGTGGCGACCTCTGAAAGCTTCTGGGCGAAGCATAT 4127
QY 4020 GTGGAATTTTCATCAGCGGGATGATATTTAGCAGGCTTGTCTGCTGCTGCGCAACCC 4079
Db 4128 GTGGAATTTTCATCAGCGGGATGATATTTAGCAGGCTTGTCTGCTGCTGCGCAACCC 4187
QY 4080 CGGATAGCATCACTGATGGCATTTACAGCTCTTATCAGCGCTCTATCAGCGCGCTCACCCACCAACA 4139
Db 4188 CGCAATAGCATCACTGATGGCATTTACAGCTCTTATCAGCGCGCTCACCCACCAACA 4247
QY 4140 TACCTCTCTGTTTAAATCTTGGGGGATGAGTGGCGGCGCAACTTGTCTCTTCCAGCGC 4199
Db 4248 TACCTCTCTGTTTAAATCTTGGGGGATGAGTGGCGGCGCAACTTGTCTCTTCCAGCGC 4307
QY 4200 TGTCTTCTGTTTCTGAGGCGCGCATCGCTGAGCGGCTGTGTCAGCAGCATAGGCTTGG 4259
Db 4308 CGTTTCGGCTTTCGTGGGCGCGCATCGCTGAGCGGCTGTGTCAGCAGCATAGGCTTGG 4367
QY 4260 GAAGTGTCTTGTGATATTTTGGCAGGTTATGGAGCAGGCTGAGGCGCGCTGCTGCTG 4319
Db 4368 GAAGTGTCTTGTGATATTTTGGCAGGTTATGGAGCAGGCTGAGGCGCGCTGCTGCTG 4427
QY 4320 CTTTAAAGTCTAGCGCGAGATGCCCTCCACCGAGGACCTGGCTTAACTACTCCTCTG 4379
Db 4428 CTTTAAAGTCTAGCGCGAGATGCCCTCCACCGAGGACCTGGCTTAACTACTCCTCTG 4487
QY 4380 TATCTCTCTCCCTGGGCGCTAGTGTGCGGGTGTGTCGCGAGGATCTGCTGCGGCA 4439
Db 4488 CATCTCTCTCTGCGCGCTGCTGCTGCGGGTGTGTCGCGAGCAATACTGCTGCGCA 4547

Db 6708 TACCTGGAAATCAAGAGAAAAACCCCATGGCTTTTCATATGACATCGCTGTTTCGACTC 6767
QY 6660 AACGGTCACTGAGATGACATCCGTTGAGAGATCAATCAACATGTTGACTGGC 6719
Db 6768 AACGGTCAACGAGAACGACATCCGTTGAGAGATCAATTTACCAATGTTGACTGGC 6827
QY 6720 CCCGAAGCCAGACAGAGCCATAGGTCGCTACAGAGCGCTTTACATCGGGGGCCCCCT 6779
Db 6828 CCCGAAGCCAGACAGAGCCATAGGTCGCTACAGAGCGCTTTATATCGGGGGTCCCTCT 6887
QY 6780 GACTAATTTCTAAGAGCGAGAACTGCGGCTATCGCGGTATCGCGGAGCGGTGTACTGAC 6839
Db 6888 GACTAATTTCTAAGAGCGAGAACTGCGGTTATCGCGGTATCGCGGAGCGGTGTACTGAC 6947
QY 6840 GACAGCTCGGTAATACCTTACATGTTACTTTGAAGCGGCTGCGGCTGTCGAGCTGC 6899
Db 6948 GACTAGCTCGGTAACACCTTACATGTTACTTTGAAGCGCTTGCAGCGCTGTCGAGCTGC 7007
QY 6900 GAAGCTCCAGAGCTGACAGTGTCTGATGCGGAGACGACCTTGTCTATCTGTGAAG 6959
Db 7008 GAAGCTCCAGAGCTGACAGTGTCTGATGCGGAGACGACCTTGTCTATCTGTGAAG 7067
QY 6960 CGCGGAGCCCAAGAGAGCGAGGAGCTTACGGGCTTTCAGGAGGCTATGACTAGATA 7019
Db 7068 CGCGGAGCCCAAGAGAGCGAGGAGCTTACGGGCTTTCAGGAGGCTATGACTAGATA 7127
QY 7020 CTCTGCCCCCTCGGGAGCCGACGATGCTGTAACACGAGTACGACTTGGAGTGTAAATCATG 7079
Db 7128 CTCTGCCCCCTCGGGAGCCGACGATGCTGTAACACGAGTACGACTTGGAGTGTAAATCATG 7187
QY 7080 CTCCTCAATGTGTAGTCCGCGACGATGCTTGGCAAAAGGTGTACTATCTCACCCG 7139
Db 7188 TTCCTCAATGTGTAGTCCGCGACGATGCTTGGCAAAAGGTGTACTATCTCACCCG 7247
QY 7140 TGACCCACACCCCTTGTGGGCGGTGCTGGGAGACAGCTAGACACACTCCAGTCAA 7199
Db 7248 TGATCCCAACCCCTTAGCACGGGTGCTGGGAGACAGCTAGACACACTCCAGTCAA 7307
QY 7200 TTCTGCTAGGCAACATCATGATGATGCGCCACCTTGTGGGAGGATGATCTGAT 7259
Db 7308 CTCTGCTAGGCAACATCATGATGATGCGCCACCTTGTGGGAGGATGATCTGAT 7367
QY 7260 GACTCAATTTCTTCCATCTCTTAGCTCAGGAACAACTTGAAAGCCCTAGATTCGA 7319
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QY 7500 TGTCCGCTAGGCTACTGTCAGGGGGGAGGCTGCCACTTGTGGCAAGTACCTCTT 7559
Db 7608 CGTCCGCTAGGCTACTGTCAGGGGGGAGGCTGCCACTTGTGGCAAGTACCTCTT 7667
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; Sequence 31, Application US/08384616
; Patent No. 5847101
; GENERAL INFORMATION:
; APPLICANT: OKAYAMA, Hiroto
; APPLICANT: FUKU, Isao
; APPLICANT: MORI, Chisato
; APPLICANT: TAKAMIZAWA, Akahisa
; APPLICANT: YOSHIDA, Iwao
; TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Armstrong, Westerman, Hattori, McLeland &
; ADDRESSEE: Naughton
; STREET: 1725 K St. N.W. Suite 1000
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 in, 1.44Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
; SOFTWARE: ASCII
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; APPLICATION NUMBER: US/08/384,616
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/769,996
; FILING DATE: 02-OCT-1991
; APPLICATION NUMBER: JP 2-167466
; FILING DATE: 25-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-230921
; FILING DATE: 31-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-305605
; FILING DATE: 09-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/635,451
; FILING DATE: 28-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens-Smith, Theresa M.
; REGISTRATION NUMBER: 36,281
; REFERENCE/DOCKET NUMBER: 900703B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 659-2930
; TELEFAX: (202) 887-0357
; TELEX: 440142
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7917 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA from genomic RNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..7862

FEATURE:		
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US-08-384-616-31		
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DB	1908	CCTCGCGCCCATACGGCTACTCCCAACAGACGCGGGCCCTACTTGGTTGATCATCAC 1967
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DB	1968	TAGCCTTACAGCGCGGACAGAACACAGCTCGAGGGGAGGTTCAGGTGGTTCACCGC 2027
QY	1920	AACCAATCTTTCTTGGGACCTGGTCAATGGGTGGTGGAGCTGTCTATCATGTGC 1979
DB	2028	HACCAATCTTTCTTGGGACCTGGTCAATGGGTGGTGGAGCTGTCTATCATGTGC 2087
QY	1980	CGGCTCAAGACCTTGGCGGCCCAAGGCCCCAATCACCCAAATGTACACCAATGTGA 2039
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QY	2040	CAGGACCTGTCGGCTGCAAGCGCCCCCGGGCGCTTCTTTGACACCATGACACCTG 2099
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QY	2100	CGGAGCTCGGACCTTTACTTGGTACAGGAGCATGCCAGTATCTTCGGTGGCGCGG 2159
DB	2208	TGGAGCTCAGACCTTTACTTGGTACAGGAGCATGCCAGTATCTTCGGTGGCGCGG 2267
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DB	2268	GGGCGACAGTAGGGGAGCTGTCTCTCCCGAGGCGCTCTCTACTTGAAGGCTCTTC 2327
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DB	2328	GGTGGTCCACTCTCTGCCCCCTCGGGGACGCTGTGGGCTATCTTTGGGCTCGCGTGTG 2387
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QY	2340	GGGTCCTCCGCTTTCACGACCACTGCTCCCTCGGCGGTACCGGACATCTTCAGGT 2399
DB	2448	GGGTCCTCCGCTTTCACGACCACTGCTCCCTCGGCGGTACCGGACATCTTCAGGT 2507
QY	2400	GGCCCATCTACAGCGCCCTACTGTAGCGGACAGACACTTAAGTGGCGGCTCGGTATGC 2459
DB	2508	GGCCCATCTACAGCTCCCACTGSCAGCGGACAGTACTAAAGTGGCGGCTCGGTATGC 2567
QY	2460	AGCCCAAGGATTAAGTGTCTTGTGAACCGCTCGTCCCGGACCTAGGTTCGG 2519
DB	2568	AGCCCAAGGATTAAGTGTCTTGTGAACCGCTCGTCCCAATCGCTCGCTTACCTTGGGTTTG 2627
QY	2520	GGGTATCTTAAGGCACATGTTATGACCTTAACATCAGAACCGGGGTAAAGGACCAT 2579
DB	2628	GGGTATCTTAAGGCACATGTTATGACCTTAACATCAGAACCGGGGTAAAGGACCAT 2687
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DB	2688	TACCAAGGCTGCCCCCTACTACGCTACTCCACTATGGCAAGTTTCTTCCGACGCTGGTTG 2747
QY	2640	CTTGGGGGCGCTTATGACATCAATAATGTATGATGAGTGCCTCACTGACTGACAC 2699
DB	2748	CTTGGGGGCGCTTATGACATCAATAATGTATGATGAGTGCCTCACTGACTGACAC 2807
QY	2700	TATCTGGCATCGGCAGTCTTGGACCAAGCGGACGCTGGAGCGGCTCGTCTG 2759

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QY	2760	GCTGCCACCGCTACGCTCCGGTCCGGTCCCGTCCCATCCAAACATCGAGGAGT 2819
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DB	2928	GGCTCTGTCTAATCTGGAGATCCCTTCTATGGCAAGGCTTCCCATCGAGGAGT 2987
QY	2880	CAAGGGGGGAGGACCTCTATTTCTGCCATTCMAAGAAATGTATGATGCTCGCGC 2939
DB	2988	CAGGGGGGAGGACCTCTATTTCTGTCTTCCAAGAAAGTGCAGAGTCCGCGC 3047
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QY	3000	CATCAAACTAGCGGAGACGCTCATTTGCTGTAGCAACGAGCTCTTAATGACGGGCTTATC 3059
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DB	3288	CGAGCGGGGAGGACTGTGTAGGGGAGGATGGGCAATTTACAGTTTGTGACTCCAGG 3347
QY	3240	AGAACGGCTCTCGGATGTTTCCATCTCGTTCTGTGCGAGTGTATGACGGGCTG 3299
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QY	3300	TGCTTTGTAGGACTCAGCGCGCGGAGACCTCAGTTAGTTTGGGCTTACCTAAACAC 3359
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QY	3420	CACCCATAGACGCGCCATTTCTTGTCCAGACTAGCAGGAGGAGAGCAACTTCCCTTA 3479
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; Sequence 31, Application US/08904686A
; Patent No. 5998130
; GENERAL INFORMATION:
; APPLICANT: OKAYAMA, Hiroto
; APPLICANT: FUKU, Isao
; APPLICANT: MORI, Chisato
; APPLICANT: TAKAMIZAWA, Akahisa
; APPLICANT: YOSHIDA, Iwao
; TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC
; TITLE OF INVENTION: CDNA AND ANTIGEN POLYPEPTIDE
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Armstrong, Westerman, Hattori, McLeand &
; ADDRESSEE: Naughton
; STREET: 1725 K St. N.W. Suite 1000
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Diskette, 3.5 in, 1.44Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/904,686A
; FILING DATE: 01-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/324,977
; FILING DATE: 18-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-167466
; FILING DATE: 25-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-230921
; FILING DATE: 31-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-305605
; FILING DATE: 09-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/099,706
; FILING DATE: 30-JUL-1993
; PRIOR APPLICATION DATA:
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; FILING DATE: 02-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/635,451
; FILING DATE: 28-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: McLeiland, Le-Nhung
; REGISTRATION NUMBER: 31,541
; REFERENCE/DOCKET NUMBER: 900703G
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 659-2930
; TELEFAX: (202) 887-0357
; INFORMATION FOR SEQ ID NO: 31:
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; LENGTH: 7917 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA from genomic RNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..7862
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..7916
; OTHER INFORMATION: /note= "sequence = 1500 - 9416 of
; OTHER INFORMATION: SEQ ID NO: 1"
; US-08-904-686A-31

Query Match 65.3%; Score 5218; DB 2; Length 7917;
Best Local Similarity 91.8%; Pred. No. 0;
Matches 5515; Conservative 0; Mismatches 495; Indels 0; Gaps 0;

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DB 2028 AACACAATCTTCTCGCGACCTGCTCAATGCGGTGCTTGGACTGTCTATCATGGTGC 2087

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QY 2040 CCAGGACCTCTGCGGCTGGCAAGCGCCCCCGGGCGCGTTCCTTGACACCATGCACCTG 2099

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DB 2268 GGGCAGACAGTAGGGGAGCCTCTCTCCCCCAAGGCGCGCTCTCTACTTGAAGGGCTCTTC 2327
QY 2220 GGGCGGTCTACCTGCTCTGCGGCTCGGGGACGCTGTGGGATCTTTTGGGCTGCGGTG 2279
DB 2328 GGGTGGTCCACTGCTCTGCGGCTCGGGGACGCTGTGGGATCTTTTGGGCTGCGGTG 2387
QY 2280 CACCCGAGGGGTGGGAAGGGGTGACTTTGTATCCCGCTCGAGTCTATGGAACACACTAT 2339
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QY	6000	GACAGGCGCTCTGATACGCGATCGCTGCGGAGGAAACCAAGTCCGATCAATGCACT	6059	Db	7188	TTCTCTCAATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	7247
Db	6108	GACAGGCGCTCTGATACGCGATCGCTGCGGAGGAAACCAAGTCCGATCAATGCACT	6167	QY	7140	TGACCCCAACACCCCTTGGCGGGCTGCGTGGGAGACAGCTAGACACTCCAGTCAA	7199
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Db	6168	GAGCAACTCTTTGCTCGCTCACCACCACTTTGCTGCTATGCTACCAACTCTCGAGCGCAAG	6227	QY	7200	TTCTGCTGCTAGGCAACATCATCATGATGATGCGCCACCTTGTGGGCAAGTATGCTGAT	7259
QY	6120	CTGCGGCGAAGAGGTACCTTTGACAGACTGCGAGTCTTGAGACCACTTACCGGGA	6179	Db	7308	CTCTGCTGCTAGGCAACATTTATGATGCTGCGCCACTTTTGTGGGCAAGTATGCTGAT	7367
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QY	6360	GTTGGAAGACACTGACACCAATTTGACACCACTTACGCGGAAATGAGTTTCTG	6419	Db	7548	TTCTATGCTCAGGAACTTTGGGTTACCGGCTTGGAGTCTGGAGACATCGGCCCAAGAG	7607
Db	6468	GCTGGAAGACACTGTCACCAATTTGACACCACTTACGCGGAAATGAGTTTCTG	6527	QY	7500	TGTCGCGCTAGGCTACTGTCCAGGGGGAGGGCTGCCACTTGTGGCAAGTACTCTT	7559
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Mon Aug 16 09:32:31 2004

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Search completed: August 12, 2004, 13:05:06
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OM nucleic - nucleic search, using sw model

Run on: August 12, 2004, 02:14:50 ; Search time 19689 Seconds
(without alignments)
17593.455 Million cell updates/sec

Title: US-10-005-469-4
Perfect score: 7992
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Searched: 3470272 seqs, 21671516995 residues
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Minimum DB seq length: 0
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Listing first 45 summaries

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- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	7982.6	99.9	7989	6	AR406043	AR406043 Sequence
3	7982.6	99.9	7989	6	AX036255	AX036255 Sequence
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5	7960.6	99.6	8001	6	AR406042	AR406042 Sequence
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8	7943	99.4	8001	6	AR406047	AR406047 Sequence
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10	7941.4	99.4	8001	6	AR406045	AR406045 Sequence
11	7941.4	99.4	8001	6	AX036257	AX036257 Sequence
12	7935	99.3	8001	6	AR406049	AR406049 Sequence
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ALIGNMENTS

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LOCUS AX739972
DEFINITION Sequence 3 from Patent WO02059321.
ACCESSION AX739972
VERSION AX739972.1 GI:30519246
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS de Francesco, R., Migliaccio, G. and Paonessa, G.
TITLE Hepatitis C virus replicons and replicon enhanced cells
JOURNAL Patent: WO 02059321-A 3 01-AUG-2002;
INSTITUTO DI RICERCHE DI BIOLOGIA MOLECOLARE P. ANGELETTI S.P.A.

AX739972 10690 bp DNA linear PAT 08-MAY-2003

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ACCESSION AR406043
VERSION AR406043.1 GI:40155170
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 7989)
AUTHORS Bartenschlager,R.
TITLE Hepatitis C virus culture system
JOURNAL Patent: US 6630343-A 10 07-OCT-2003;
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ORIGIN
Query Match 99.9%; Score 7982.6; DB 6; Length 7989;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 7985; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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 Qy 601 CGACGGGCTTCTTTCGCGAGCTGTCTGAGCTTGTCTGAGCGGAGGAGGCTGGC 660
 Db 601 CGACGGGCTTCTTTCGCGAGCTGTCTGAGCTTGTCTGAGCGGAGGAGGCTGGC 660
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 Db 661 TGTATTTGGCGGAAGTGCAGGGGAGGATCTCTGTCACTCACTTGTCTTCTGCGAGA 720
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 Db 721 AAGTATCCATATGCTGATGAAATGCGGCTGATAGCTTGTATCGGCTACCTGCTG 780
 Qy 781 CATTCGACCAACGAGCAATCTGATCGAGGAGCAGTCTCGATGGAAGCGGCTC 840
 Db 781 CATTCGACCAACGAGCAATCTGATCGAGGAGCAGTCTCGATGGAAGCGGCTC 840
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 Db 841 TTGTCGATCAGGATGATCTGAGCAAGAGCATCAGGGGCTCGCGCCAGCGAATCTGTTCG 900
 Qy 901 CGAGGCTCAAGGCGGATGCCGAGGATCTCGTGTGACCCATGGCGATGCTCCT 960
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 Db 1021 TGGGTGTGGCGGACCGCTATCAGGACATAGCTTGGCTACCGGTGATTTGCTGAGAGC 1080
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 Db 1081 TTGGCGGCAATGGGCTGAGCGCTTCTCGTGTACGCTATCGCGCTCCCGATTCGC 1140
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 Db 1141 AGCGCATGCGCTTCTATCGCTTCTTGAAGAGTCTTCTGAGTTTAAACAGACCAACG 1200
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 Qy 1861 AGCCTCAGAGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1920
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 Qy 2281 ACCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2340
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QY	2341	CGTCCCCGGTCTTCAOGGACAACTCGTCCCTCCGGCGTACCGCAGACATTCAGGTG	2400	Db	3421	ACCCACATAGACGCCCATTTCTTTGCCAGATAAGCAGGCGAGGACAACTTCCCTAC	3480
Db	2341	CGTCCCCGGTCTTCAOGGACAACTCGTCCCTCCGGCGTACCGCAGACATTCAGGTG	2400	QY	3481	CTGGTAGCATACCAAGCTACCGGTGTGCGCCAGGGCTCAGGGCTCCACCTCCATCTGTTGGAC	3540
QY	2401	GCCCATCTACACGCCCTTACTGGTAGCGCAAGAGCACTAAGGTGCGGCTCGGTATGCA	2460	Db	3481	CTGGTAGCATACCAAGCTACCGGTGTGCGCCAGGGCTCAGGGCTCCACCTCCATCTGTTGGAC	3540
Db	2401	GCCCATCTACACGCCCTTACTGGTAGCGCAAGAGCACTAAGGTGCGGCTCGGTATGCA	2460	QY	3541	CAATGTGGAAGTGTCTCATACGGCTAAAGCTACGCTGCACGGGCCCAACGCCCTGCTG	3600
QY	2461	GCCCAAGGATTAAGTGTCTCTGAAACCGCTCCGTCCGCCGCCACCTAGTTTCGGG	2520	Db	3541	CAATGTGGAAGTGTCTCATACGGCTAAAGCTACGCTGCACGGGCCCAACGCCCTGCTG	3600
Db	2461	GCCCAAGGATTAAGTGTCTCTGAAACCGCTCCGTCCGCCGCCACCTAGTTTCGGG	2520	QY	3601	TATAGCTGGAGCGGTTCAAAACGAGGTACTACACACACCCCATACCAATAATATC	3660
QY	2521	GCGTATATGTCTAAGGCACTGTTATCGACCTTAACTAATCAGAACCGGGGTAAAGACCAT	2580	Db	3601	TATAGCTGGAGCGGTTCAAAACGAGGTACTACACACACCCCATACCAATAATATC	3660
Db	2521	GCGTATATGTCTAAGGCACTGTTATCGACCTTAACTAATCAGAACCGGGGTAAAGACCAT	2580	QY	3661	ATGGCATCATGTGCGGTGACCTGGAGGTCTGTCAGAGCACTGGGTGCTGTAGGCGGA	3720
QY	2581	ACCCGGGTGCCCCATCAGTACTCCACTATGCAAGTATGCAAGTATTCGCGGAGGTGTC	2640	Db	3661	ATGGCATCATGTGCGGTGACCTGGAGGTCTGTCAGAGCACTGGGTGCTGTAGGCGGA	3720
Db	2581	ACCCGGGTGCCCCATCAGTACTCCACTATGCAAGTATGCAAGTATTCGCGGAGGTGTC	2640	QY	3721	GTCTTAGCAGCTCTGGCCCGCTATTGCTGACACAGCAGCGTGTCAATTGTGGGCAAG	3780
QY	2641	TCTGGGGCGGCTATGACATCATATATGTGATGAGTCCCACTCAACTGACTCGACCACT	2700	Db	3721	GTCTTAGCAGCTCTGGCCCGCTATTGCTGACACAGCAGCGTGTCAATTGTGGGCAAG	3780
Db	2641	TCTGGGGCGGCTATGACATCATATATGTGATGAGTCCCACTCAACTGACTCGACCACT	2700	QY	3781	ATCATCTTGTCCGGAAGCGCGGCATCATTCGCCGACAGGGAAGTCTTTTACCGGAGTTC	3840
QY	2701	ATCTGGGCGATGGCAGTCTCTGGACCAAGCGGAGCGGTGGAGCGGACTCGTCTGTG	2760	Db	3781	ATCATCTTGTCCGGAAGCGCGGCATCATTCGCCGACAGGGAAGTCTTTTACCGGAGTTC	3840
Db	2701	ATCTGGGCGATGGCAGTCTCTGGACCAAGCGGAGCGGTGGAGCGGACTCGTCTGTG	2760	QY	3841	GATGAGATGGAAGAGTGGCCTCACACCTCCCTTACATCGAACAGGGAATCAGCTGCC	3900
QY	2761	CTCGCCACCGTACGCTCCGGGATCGTCAAGTGCACATCCAAATCGAGAGGTG	2820	Db	3841	GATGAGATGGAAGAGTGGCCTCACACCTCCCTTACATCGAACAGGGAATCAGCTGCC	3900
Db	2761	CTCGCCACCGTACGCTCCGGGATCGTCAAGTGCACATCCAAATCGAGAGGTG	2820	QY	3901	GAACAATTCAAACAGAGAGGCAATCGGTGTGTCGAAACAGCCACCAAGCAGGAGGCT	3960
QY	2821	GCTCTGTCCAGCACTGGAGAAATCCCTTTTATGCAAGAGCCATCCCATCGAGACCATC	2880	Db	3901	GAACAATTCAAACAGAGAGGCAATCGGTGTGTCGAAACAGCCACCAAGCAGGAGGCT	3960
Db	2821	GCTCTGTCCAGCACTGGAGAAATCCCTTTTATGCAAGAGCCATCCCATCGAGACCATC	2880	QY	3961	GCTCTCCGTGTGGTAAATCCAGTGGGAGCCCTCGAAGCCTTCTGGGCGAAGATATG	4020
QY	2881	AAGGGGGAGGACCTCATTTCTGCCATTCGAAGAAATGTGATGAGCTCGCCGCG	2940	Db	3961	GCTCTCCGTGTGGTAAATCCAGTGGGAGCCCTCGAAGCCTTCTGGGCGAAGATATG	4020
Db	2881	AAGGGGGAGGACCTCATTTCTGCCATTCGAAGAAATGTGATGAGCTCGCCGCG	2940	QY	4021	TGGAATTCATCAGCGGATACAAATATTTAGCAGGCTTTGTCACCTCTGCTGCGCAACCC	4080
QY	2941	AAGCTGTCCGCTCGGACTCAATGTCTGTAGCATATTAACCGGGCCCTTGATATCCGTC	3000	Db	4021	TGGAATTCATCAGCGGATACAAATATTTAGCAGGCTTTGTCACCTCTGCTGCGCAACCC	4080
Db	2941	AAGCTGTCCGCTCGGACTCAATGTCTGTAGCATATTAACCGGGCCCTTGATATCCGTC	3000	QY	4081	GCGATAGCATCTGATGGCATTCACAGCCTTATACACGCGGCTCACCAACCAACAT	4140
QY	3001	ATACCAACTAGCGAGAGCTCATTTCTGTAGCAATACATGTCTCAACAGACAGTTCAGC	3060	Db	4081	GCGATAGCATCTGATGGCATTCACAGCCTTATACACGCGGCTCACCAACCAACAT	4140
Db	3001	ATACCAACTAGCGAGAGCTCATTTCTGTAGCAATACATGTCTCAACAGACAGTTCAGC	3060	QY	4141	ACCTCTCTTTTAAACATCTCGGGGGATGGTGGCGGCCAACTTGTCTCTCCAGCGCT	4200
QY	3061	GGCGATTTGACCTCAGTGATCGACTGCAATACATGTCTCAACAGACAGTTCAGC	3120	Db	4141	ACCTCTCTTTTAAACATCTCGGGGGATGGTGGCGGCCAACTTGTCTCTCCAGCGCT	4200
Db	3061	GGCGATTTGACCTCAGTGATCGACTGCAATACATGTCTCAACAGACAGTTCAGC	3120	QY	4201	GCTTCTGCTTTAGCGCGGCTATCGCTGGAGCGGCTGTGGCAGCATAGGCTTTGGG	4260
QY	3121	CTGACCGGACCTTACCATTTGAGACAGACCGTGCACAGACGGGTGTCAAGCTCG	3180	Db	4201	GCTTCTGCTTTAGCGCGGCTATCGCTGGAGCGGCTGTGGCAGCATAGGCTTTGGG	4260
Db	3121	CTGACCGGACCTTACCATTTGAGACAGACCGTGCACAGACGGGTGTCAAGCTCG	3180	QY	4261	AAGGTGCTTGTGATATTTTGGCAGGTTATGAGCAGGGGTGGCAGCGGCTCGTGCC	4320
QY	3181	CAGCGGCGAGGACGAGTGTAGGGGAGGATGGGCAATTTACAGGTTTGTGACTCCAGGA	3240	Db	4261	AAGGTGCTTGTGATATTTTGGCAGGTTATGAGCAGGGGTGGCAGCGGCTCGTGCC	4320
Db	3181	CAGCGGCGAGGACGAGTGTAGGGGAGGATGGGCAATTTACAGGTTTGTGACTCCAGGA	3240	QY	4321	TTTAAAGTATAGCGCGGATGCGCTCCACCGAGGACCTGGCTAACCTACTCCCTGT	4380
QY	3241	GAAACCGGCTCGGGCATGTTGATCTCGGTTCTGTGCGAGTGTCTATGACGGGGCTGT	3300	Db	4321	TTTAAAGTATAGCGCGGATGCGCTCCACCGAGGACCTGGCTAACCTACTCCCTGT	4380
Db	3241	GAAACCGGCTCGGGCATGTTGATCTCGGTTCTGTGCGAGTGTCTATGACGGGGCTGT	3300	QY	4381	ATCCTCTCCCTCGGCGGCTTAGTCTGGGGTCTGTGGCGCAGCGATACTGCGTCGGCAC	4440
QY	3301	GCTTGTAGCAGCTCAGCGCGCGGAGACCTCAGTTAGTTGGGGCTTACCTTAAACACA	3360	Db	4381	ATCCTCTCCCTCGGCGGCTTAGTCTGGGGTCTGTGGCGCAGCGATACTGCGTCGGCAC	4440
Db	3301	GCTTGTAGCAGCTCAGCGCGCGGAGACCTCAGTTAGTTGGGGCTTACCTTAAACACA	3360	QY	4441	GTGGCGGCGAGGAGGGGCTGTGAGTGTGATGAACCGGCTGATAGCGTTTCGCTTCGCGG	4500
QY	3361	CCAGGTTGCGGCTCTGCCAGGACCATCTCGAGTTCTGTGGAGAGCGCTTTTACAGGCTC	3420	Db	4441	GTGGCGGCGAGGAGGGGCTGTGAGTGTGATGAACCGGCTGATAGCGTTTCGCTTCGCGG	4500
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QY	3421	ACCCACATAGACGCCCATTTCTTTGCCAGATAAGCAGGCGAGGACAACTTCCCTAC	3480				

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Qy 4561 CAGATCCTCTCTAGTCTTACCATCACTCAGCTGCTGAAGAGGCTTCAACAGTGGATCAAC 4620
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AX036255
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ACCESSION AX036255
VERSION AX036255.1 GI:11225871
KEYWORDS
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
Virus; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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REFERENCE 1
AUTHORS Bartenschlager,R.D.
TITLE Hepatitis c virus cell culture system
JOURNAL Patent: EP 1043399-A 4 11-OCT-2000;
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RESULT 4

RESULI 4
SSE242652

SSE242652
LOCUS

LOCUS
DEFINITION

DEFINITION Hepatitis C virus replicon I377/NS3-3'UTR.

1. The first step is to identify the problem or question that needs to be answered. This involves understanding the context and the specific requirements of the task.

AJ242652
 VERSION
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 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 MEDLINE
 PUBMED
 REFERENCE
 AUTHORS
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 JOURNAL
 FEATURES
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 CDS
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AJ242652.1 GI:5441834
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 Hepatitis C virus replicon I377/NS3-3'UTR
 Hepatitis C virus replicon I377/NS3-3'UTR
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 Lohmann,V., Korner,F., Koch,J., Herian,U., Theilmann,L. and Bartenschlager,R.
 Replication of subgenomic hepatitis C virus RNAs in a hepatoma cell line
 Science 285 (5424), 110-113 (1999)
 9930360
 2 (bases 1 to 7989)
 Bartenschlager,R.
 Direct Submission.
 Submitted (26-MAY-1999) Bartenschlager R., Institute for Virology, Johannes Gutenberg - University Mainz, Obere Zahlbacher Strasse 67, 55131 Mainz, GERMANY
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99.9%; ity servative	Score Pred. No. 0; 0; Mismatches	DB 12; 4; Indels	Length 7989; 0; Gaps
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Db		
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Db		

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DB |||||
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QY 2689 GACTCGAACCACTATCTCTGGGCGATCGGCACAGTCTTGACCAAGCGGAGACGGCTGAGCG 2748
DB |||||
2701 GACTCGAACCACTATCTCTGGGCGATCGGCACAGTCTTGACCAAGCGGAGACGGCTGAGCG 2760
QY 2749 CGACTCGTCTGCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2808
DB |||||
2761 CGACTCGTCTGCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2820
QY 2809 ATCGAGGAGGTGGCTCTCTCGAGCACTGGAGAAATCCCTTTTATGGGAAAGCCATCC 2868
DB |||||
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QY 2869 ATCGAGGAGGTGGCTCTCTCGAGCACTGGAGAAATCCCTTTTATGGGAAAGGTGTAT 2928
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2881 ATCGAGGAGGTGGCTCTCTCGAGCACTGGAGAAATCCCTTTTATGGGAAAGGTGTAT 2940
QY 2929 GAGCTCGCGGCGGAGGCTCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2988
DB |||||
2941 GAGCTCGCGGCGGAGGCTCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3000
QY 2989 GATGATCCGTCTATACCAACTAGCGGAGACGCTCATTTCTGCCATTTCCAAAGAAATGTAT 3048
DB |||||
3001 GATGATCCGTCTATACCAACTAGCGGAGACGCTCATTTCTGCCATTTCCAAAGAAATGTAT 3060
QY 3049 ACGGGCTTTACCGGCGATTTTCGACTAGTGTATCGACTGATGTGTGTCACCCAGACA 3108
DB |||||
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QY 3109 GTCCGACTTACGCTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3168
DB |||||
3121 GTCCGACTTACGCTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3180
QY 3169 GTGTCACGCTCGCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3228
DB |||||
3181 GTGTCACGCTCGCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3240
QY 3229 GTGACTCCAGGAGAACGGCGCTCGGGCATGTTTGGATTTCTCGGTTCTGTGCGAGTGTAT 3288
DB |||||
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QY 3289 GAGCGGCGGCTGCTGTTGTTAGTACGAGCTCACCGCGCGGCGGCGGCGGCGGCGG 3348
DB |||||
3301 GAGCGGCGGCTGCTGTTGTTAGTACGAGCTCACCGCGCGGCGGCGGCGGCGGCGG 3360
QY 3349 TACTTAAACACACAGGCTTCCCGCTCTGCGAGGACCATCTGAGTTCTGCGAGAGGCTC 3408
DB |||||
3361 TACTTAAACACACAGGCTTCCCGCTCTGCGAGGACCATCTGAGTTCTGCGAGAGGCTC 3420
QY 3409 TTTTACAGGCTCACCCACATAGAGCGGCGGCTTTCTTGTCCAGACTAAGCAGGCGGAGAC 3468
DB |||||
3421 TTTTACAGGCTCACCCACATAGAGCGGCGGCTTTCTTGTCCAGACTAAGCAGGCGGAGAC 3480
QY 3469 AACTTCCCTTACCTGTAGCATACAGGCTACCGGTGTGCGGCGGCGGCGGCGGCGG 3528
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DB |||||
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QY 3589 AGCGGCTTCTGTATAGGCTGGGAGCGGCTTCAAAAAGAGGTACTACCACACACCCCAT 3648
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QY 3649 ACCAAATACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3708
DB |||||
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QY 3709 CTGGTGGGCGGAGTCTTACGAGCTCTGGCGGCGGCTATTGCTGACAAACAGGCGGCTG 3768
DB |||||
3721 CTGGTGGGCGGAGTCTTACGAGCTCTGGCGGCGGCTATTGCTGACAAACAGGCGGCTG 3780
QY 3769 ATTGGGCGGAGGATCATCTTGTCCGGAGAGCGGCGGCGGCTATTCCCGACAGGAGGCTCT 3828

QY	5989	TCCTACACATGGACAGGCGCCCTTGATCAGCCCATGCGCTCGGAGGAAAAACAAGCTGCC	6048
Db	6001	TCCTACACATGGACAGGCGCCCTTGATCAGCCCATGCGCTCGGAGGAAAAACAAGCTGCC	6060
QY	6049	ATCAATGCACGTAGCAACTCTTTTGGCTCGGTCAACCAAACTTGGTCTATGCTTACAACAATCT	6108
Db	6061	ATCAATGCACGTAGCAACTCTTTTGGCTCGGTCAACCAAACTTGGTCTATGCTTACAACAATCT	6120
QY	6109	CGCAGCGCAAGCCTTCGCGCAAGAAAGTTCACCTTTGACAGACTGCAGGTCTCTGGACAC	6168
Db	6121	CGCAGCGCAAGCCTTCGCGCAAGAAAGTTCACCTTTGACAGACTGCAGGTCTCTGGACAC	6180
QY	6169	CACCTACCGGACGTCTCAAGGAGATGAAGCGAAGGCGTCCACAGTTAAGCTTAAACTT	6228
Db	6181	CACCTACCGGACGTCTCAAGGAGATGAAGCGAAGGCGTCCACAGTTAAGCTTAAACTT	6240
QY	6229	CTATCCGTGGAGGAAGCTGTAAAGCTGACGCCGCCACATTCGGCCAGATCTAAATTTGGC	6288
Db	6241	CTATCCGTGGAGGAAGCCTGTAAAGCTGACGCCGCCACATTCGGCCAGATCTAAATTTGGC	6300
QY	6289	TATGGGCAAGAGACGTCCGGAACCTATCAGCAAGCGCGTTAACACATCCCGTCCGCTG	6348
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QY	6349	TGGAAAGACTTGTGGAAGACACTGACACACCAANTTCACACACCAATCATGGCAAAAAAT	6408
Db	6361	TGGAAAGACTTGTGGAAGACACTGACACACCAANTTCACACACCAATCATGGCAAAAAAT	6420
QY	6409	GAGGTTTTCTGCGTCCAAACAGAGAAAGGGGGCGCAAGCAGCTCGCTTTATCGTATTTC	6468
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QY	6469	CCAGATTGGGGGTTCTGTGTGCGAGAAATAAGCCCTTTACGATGGGTCTCCACCCCTC	6528
Db	6481	CCAGATTGGGGGTTCTGTGTGCGAGAAATAAGCCCTTTACGATGGGTCTCCACCCCTC	6540
QY	6529	CCTCAGSCCGTGATGGGCTCTTCATACGGATTCCAATACTCTCTCGACAGCGGTCGAG	6588
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QY	6589	TTCTGTGTGAATGCCTCGAAAGCGAAATAAGCCCTATGGGCTTCGCAVATGACACCCGC	6648
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QY	6649	TGTTTTGACTCAACGGTCACTGAGATGACATCGGTGTGAGAGTCAATCTACCAATGT	6708
Db	6661	TGTTTTGACTCAACGGTCACTGAGATGACATCGGTGTGAGAGTCAATCTACCAATGT	6720
QY	6709	TGTGACTTGGCCCCCGAAGCGACAGCGGCATAAGGTGCGCTCACAGAGCGGCTTTACATC	6768
Db	6721	TGTGACTTGGCCCCCGAAGCGACAGCGGCATAAGGTGCGCTCACAGAGCGGCTTTACATC	6780
QY	6769	GGGGCCCCCTGACTAATTTCAAAGGCGAAACTGCGGCTATCCCGGTCGCGCGGAGC	6828
Db	6781	GGGGCCCCCTGACTAATTTCAAAGGCGAAACTGCGGCTATCCCGGTCGCGCGGAGC	6840
QY	6829	GGTGTACTGACGACACGCTCGGTGTAATACCCCTCACATGTTTACTTGAAGCGCGTCGGCC	6888
Db	6841	GGTGTACTGACGACACGCTCGGTGTAATACCCCTCACATGTTTACTTGAAGCGCGTCGGCC	6900
QY	6889	TGTCGAGCTCGAAGCTCCAGGACTGCACATGCTCGTATGCGGAGACGACCTTGTGCTT	6948
Db	6901	TGTCGAGCTCGGAGCTTCAGGACTGCACATGCTCGTATGCGGAGACGACCTTGTGCTT	6960
QY	6949	ATCTGTGAAAGCGCGGGAACCCAAAGGACGAGCGCCTACGGGCTTTCACGAGGCT	7008
Db	6961	ATCTGTGAAAGCGCGGGAACCCAAAGGACGAGCGCCTACGGGCTTTCACGAGGCT	7020
QY	7009	ATGACTAGATACTCTGCCCCCTCGGGACCGCGCCAAACAGAAATACGACTTGGAGTTG	7068
Db	7021	ATGACTAGATACTCTGCCCCCTCGGGACCGCGCCAAACAGAAATACGACTTGGAGTTG	7080

QY	7069	ATATCATCATGCTCTCTCCATATGTGTCTAGTCCGCGACGATGCATCTGGCAAAAGGGTGTAC	7129
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QY	7129	TATCTCACCGGTGACCCACACCCCTTGGCGGGCTGGTGGGAGACAGCTAGACAC	7188
Db	7141	TATCTCACCGGTGACCCACACCCCTTGGCGGGCTGGTGGGAGACAGCTAGACAC	7200
QY	7189	ACTCCAGTCAATTTCTGGCTAGGCAACATCATGTATGCGGCCACCTTGTGGGCAAGG	7248
Db	7201	ACTCCAGTCAATTTCTGGCTAGGCAACATCATGTATGCGGCCACCTTGTGGGCAAGG	7260
QY	7249	ATGATCTGATGACTCATTTCTTCTTCATCCCTTCTAGCTCAGAAACAATTGAAAAGCC	7308
Db	7261	ATGATCTGATGACTCATTTCTTCTTCATCCCTTCTAGCTCAGAAACAATTGAAAAGCC	7320
QY	7309	CTAGATGTCAGATCTACGGGGCTGTATTCTCCATTGAGCCACTTGACCTACCTCAGATC	7368
Db	7321	CTAGATGTCAGATCTACGGGGCTGTATTCTCCATTGAGCCACTTGACCTACCTCAGATC	7380
QY	7369	ATTCAACGACTCCATGGCCCTTAGCGCAATTTTCTACTCCATAGTTTACTTCTCCAGGTGAGATC	7428
Db	7381	ATTCAACGACTCCATGGCCCTTAGCGCAATTTTCTACTCCATAGTTTACTTCTCCAGGTGAGATC	7440
QY	7429	AATAGGGTGGCTTTCATGCCCTCAGGAAACTTTGGGGTACCGCCCTTGGAGTCTCGAGACAT	7488
Db	7441	AATAGGGTGGCTTTCATGCCCTCAGGAAACTTTGGGGTACCGCCCTTGGAGTCTCGAGACAT	7500
QY	7489	CGGGCCAGAAGTGTCCGCGCTAGGCTACTGTGCCAGGGGGGAGAGGCTGCACTTGTGGC	7548
Db	7501	CGGGCCAGAAGTGTCCGCGCTAGGCTACTGTGCCAGGGGGGAGAGGCTGCACTTGTGGC	7560
QY	7549	AAGTACCTCTTCAACTGGGCAGTAGAGCAACAAGCTCAAACTCACTCCACTCCCGGCTGGG	7608
Db	7561	AAGTACCTCTTCAACTGGGCAGTAGAGCAACAAGCTCAAACTCACTCCACTCCCGGCTGGG	7620
QY	7609	TCCAGTTGGATTTATCCAGCTGGTTCTGTTCTGTTTACAGCGGGGGAGACATATATCAC	7668
Db	7621	TCCAGTTGGATTTATCCAGCTGGTTCTGTTCTGTTTACAGCGGGGGAGACATATATCAC	7680
QY	7669	AGCTGTCTCGTGGCGGACCCCGCTGGTTCATGTGTGCTTACTCTTCTTCTGTAGGG	7728
Db	7681	AGCTGTCTCGTGGCGGACCCCGCTGGTTCATGTGTGCTTACTCTCTTCTGTAGGG	7740
QY	7729	GTAGGCATCTACTCTCCCAACCGATGAAACGGGAGCTAAACACTCCAGGCCAATAGG	7788
Db	7741	GTAGGCATCTACTCTCCCAACCGATGAAACGGGAGCTAAACACTCCAGGCCAATAGG	7800
QY	7789	CCATCTCTGTTTTTTTCCCTTT	7848
Db	7801	CCATCTCTGTTTTTTTCCCTTT	7860
QY	7849	TTTTCTCTTTTTTTTTTTTTCCTTTTTTTTTTTTCTTTTCTTTCTTTGTTGGTTCACCTTAGC	7908
Db	7861	TTTTCTCTTTTTTTTTTTTTCCTTTTTTTTTTTTCTTTTCTTTCTTTGTTGGTTCACCTTAGC	7920
QY	7909	CCTAGTCAGGCTAGCTGTGAAGTCCCGTGGCCGCTTGAATGACAGAGTGTCTGATAC	7968
Db	7921	CCTAGTCAGGCTAGCTGTGAAGTCCCGTGGCCGCTTGAATGACAGAGTGTCTGATAC	7980
QY	7969	TGGCCCTCTCTGCAGATCAAGT 7989	
Db	7981	TGGCCCTCTCTGCAGATCAAGT 8001	
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AX036254			
LOCUS	AX036254 8001 bp DNA linear PAT 16-NOV-2000		
DEFINITION	Sequence 3 from Patent EP1043399.		
ACCESSION	AX036254		
VERSION	AX036254.1 GI:11225870		
KEYWORDS	Hepatitis C virus		
SOURCE			

RESULT 6
AX036254
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE

ORGANISM	Hepatitis C virus	Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.
REFERENCE	1	
AUTHORS	Bartenschlager, R.D.	
TITLE	Hepatitis C virus cell culture system	
JOURNAL	Patent: EP 1043399-A 3 11-OCT-2000;	
	BARTENSCHLAGER RALF DR (DE)	
FEATURES	Location/Qualifiers	
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	/mol_type="unassigned DNA"	
	/db_xref="taxon:11103"	
ORIGIN		
	Query Match 99.6%; Score 7960.6; DB 6; Length 8001;	
	Best Local Similarity 99.8%; Pred. No. 0;	
	Matches 7985; Conservative 0; Mismatches 4; Indels 12; Gaps 1;	
QY	1	GCACGCCCGGATGGGGGCGACACTCCACATAGATCACTCCCTGTGAGGAATCTG 60
DB	1	GCACGCCCGGATGGGGGCGACACTCCACATAGATCACTCCCTGTGAGGAATCTG 60
QY	61	TCTTCACGAGAAAGCGTCTAGCCATGGCGTTAGTATGAGTGTGCGAGCCTCCAGGAC 120
DB	61	TCTTCACGAGAAAGCGTCTAGCCATGGCGTTAGTATGAGTGTGCGAGCCTCCAGGAC 120
QY	121	CCCCCTCCGGAGAGCCATAGTGGTCTGGGAACCGGTAGTATGAGTGTGCGAGCCTCCAGGAC 180
DB	121	CCCCCTCCGGAGAGCCATAGTGGTCTGGGAACCGGTAGTATGAGTGTGCGAGCCTCCAGGAC 180
QY	181	GACGACGGGTCTTCTTGGATCAACCGCTCAATGCTGAGATTTGGGGTGCCCC 240
DB	181	GACGACGGGTCTTCTTGGATCAACCGCTCAATGCTGAGATTTGGGGTGCCCC 240
QY	241	GGGAGCTCTAGCCGAGTAGTGTGGGTGCGAAAGGCTTGTGCTATGCTGATAGG 300
DB	241	GGGAGCTCTAGCCGAGTAGTGTGGGTGCGAAAGGCTTGTGCTATGCTGATAGG 300
QY	301	GTGCTTGGAGTGTCCCGGAGGCTCTGAGACCGGTGACACCGGTGACGAAATCTCTAAAC 360
DB	301	GTGCTTGGAGTGTCCCGGAGGCTCTGAGACCGGTGACACCGGTGACGAAATCTCTAAAC 360
QY	361	CTCAAGAAACCAAA-----GGCGCGCCATGATGAACAAAGATGATTCG 408
DB	361	CTCAAGAAACCAAA-----GGCGCGCCATGATGAACAAAGATGATTCG 420
QY	409	ACGAGGTTCTCCGGCGCTTGGGTGGAGAGGCTATTCGGCTATGACTGGGCAACAGA 468
DB	421	ACGAGGTTCTCCGGCGCTTGGGTGGAGAGGCTATTCGGCTATGACTGGGCAACAGA 480
QY	469	CAATCGGTCTCTGATCGCGCGTGTTCGGCTGTGAGGAGGCGCGGCTCTTT 528
DB	481	CAATCGGTCTCTGATCGCGCGTGTTCGGCTGTGAGGAGGCGCGGCTCTTT 540
QY	529	TTGTCAAGACCGACTCTCCGGTCCCTGAATGAAGTCTGAGGAGGCGCGGCTAT 588
DB	541	TTGTCAAGACCGACTCTCCGGTCCCTGAATGAAGTCTGAGGAGGCGCGGCTAT 600
QY	589	CGTGGCTGGCCACGAGCGCGTTCCTTGGCGAGCTGTGCTGCAAGTGTCTCTGAGAGCGG 648
DB	601	CGTGGCTGGCCACGAGCGCGTTCCTTGGCGAGCTGTGCTGCAAGTGTCTCTGAGAGCGG 660
QY	649	GAGGAGCTGGTCTATTGGCGAGTGGCGGCGAGGATCTCTGCTATCTCACTTGG 708
DB	661	GAGGAGCTGGTCTATTGGCGAGTGGCGGCGAGGATCTCTGCTATCTCACTTGG 720
QY	709	CTCCTCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGGCGGCTGCAAGCTTGATC 768
DB	721	CTCCTCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGGCGGCTGCAAGCTTGATC 780
QY	769	CGGCTACTGCTCCATTCGACCAACGAAACATCGCATGAGCGAGCAGCTACTCGGA 828

Db	781	CGGTACTCCTGCCATTCGACCAACCAAGCGAAACATCGCATCGAGCGAGCAGTACTCGGA 840
QY	829	TGGAGCCGGTCTTGTGATCAGGATGATCTGGAGAGAGCATCAGGGGCTCGGCCAG 888
Db	841	TGGAGCCGGTCTTGTGATCAGGATGATCTGGAGAGAGCATCAGGGGCTCGGCCAG 900
QY	889	CCGAATCTTCCGCGAGGCTCAAGCGCGCATCGCCGAGGAGATCTCGTCTGACCC 948
Db	901	CCGAATCTTCCGCGAGGCTCAAGCGCGCATCGCCGAGGAGATCTCGTCTGACCC 960
QY	949	ATGCGATGCTGCTGCTGCGAATATCATGTGAGAAATATGCGCGCTTTTCTGATTCATCG 1008
Db	961	ATGCGATGCTGCTGCTGCGAATATCATGTGAGAAATATGCGCGCTTTTCTGATTCATCG 1020
QY	1009	ACTGTGGCGGCTGGTGTGGGACCGCTATCAGGACATAGCGTGGCTACCGGTGATA 1068
Db	1021	ACTGTGGCGGCTGGTGTGGGACCGCTATCAGGACATAGCGTGGCTACCGGTGATA 1080
QY	1069	TTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCTCTGCTTTTACGGTATCGCG 1128
Db	1081	TTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCTCTGCTTTTACGGTATCGCG 1140
QY	1129	CTCCGATTCGAGCGGATCGCTTCTATCGCTTCTTGAAGAGTCTCTGAGTTTAA 1188
Db	1141	CTCCGATTCGAGCGGATCGCTTCTATCGCTTCTTGAAGAGTCTCTGAGTTTAA 1200
QY	1189	CAGACCAACCGTTTCCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCT 1248
Db	1201	CAGACCAACCGTTTCCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCT 1260
QY	1249	AACTTACTTGGCGAAGCGCTTGAATTAAGCGCGTGTGCGTTTGTCTATATGTTAT 1308
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QY	1309	TCACCATATTCGCGCTTTTGGCAATGTGAGGCGCGGAAACCTGGCCCTCTCTCTG 1368
Db	1321	TCACCATATTCGCGCTTTTGGCAATGTGAGGCGCGGAAACCTGGCCCTCTCTCTG 1380
QY	1369	ACGACATTCCTAGGGGTCTTTCGCTCTCGCAAGGAATCAAGGTCTGTGATGATGTC 1428
Db	1381	ACGACATTCCTAGGGGTCTTTCGCTCTCGCAAGGAATCAAGGTCTGTGATGATGTC 1440
QY	1429	GTGAAGGAGCAGTTCTCTGGAAGCTTCTTGAAGCAACCAACGCTGTAGCGACCTT 1488
Db	1441	GTGAAGGAGCAGTTCTCTGGAAGCTTCTTGAAGCAACCAACGCTGTAGCGACCTT 1500
QY	1489	TGCGAGCGGAAACCCCGCTCTGCGACAGTGCCTCTGCGGCAAGGCAAGCAGTCTA 1548
Db	1501	TGCGAGCGGAAACCCCGCTCTGCGACAGTGCCTCTGCGGCAAGGCAAGCAGTCTA 1560
QY	1549	TAAGATACACCTGCAAGCGCGCAACCCCGCTGCGAGTGTGAGTTGAGTGTG 1608
Db	1561	TAAGATACACCTGCAAGCGCGCAACCCCGCTGCGAGTGTGAGTTGAGTGTG 1620
QY	1609	GAAAGAGTCAATGCTCTCTCAAGCGTATTCAACAGGGGCTGAAGGATCCGAGAG 1668
Db	1621	GAAAGAGTCAATGCTCTCTCAAGCGTATTCAACAGGGGCTGAAGGATCCGAGAG 1680
QY	1669	GTACCCCATTTGATGGGATCTGATCTGGGCTCGGTGACATGCTTTACATGTTTGTAG 1728
Db	1681	GTACCCCATTTGATGGGATCTGATCTGGGCTCGGTGACATGCTTTACATGTTTGTAG 1740
QY	1729	TCGAGTTAAAAAAGTCTTAGGCCCCCGAAACGAGGGGACGTGGTTTTCTTTGAAAAA 1788
Db	1741	TCGAGTTAAAAAAGTCTTAGGCCCCCGAAACGAGGGGACGTGGTTTTCTTTGAAAAA 1800
QY	1789	CACGATAATACATGCGGCTATTACGGCTTACTCCAAACAGACGGGAGGCTTCTGCG 1848
Db	1801	CACGATAATACATGCGGCTATTACGGCTTACTCCAAACAGACGGGAGGCTTCTGCG 1860
QY	1849	TGCATCATCATGCTCTACAGCGGGGACAGAACAGGTGAGGGGAGGTCAGAGGTG 1908
Db	1861	TGCATCATCATGCTCTACAGCGGGGACAGAACAGGTGAGGGGAGGTCAGAGGTG 1920

Q/	1909	GTCTCCACCGCAACACAAATCTTTCTGTGGCAGCTCGTCAATGGCGTGTGTGGACTGTC	1968	Q/	2989	GATGTATCCGTATACCAACTAGCGGAGACGCTCATTTCTGTAGCAACGAGCGCTTAATG	3048
D/	1971	GTCTCCACCGCAACACAAATCTTTCTGTGGCAGCTCGTCAATGGCGTGTGTGGACTGTC	1980	D/	3001	GATGTATCCGTATACCAACTAGCGGAGACGCTCATTTCTGTAGCAACGAGCGCTTAATG	3060
Q/	1969	TATCATGGTGGCGGTCAAAGACCTTTGCGGCGCAAAAGGCGCCCAATCACCCAAATGTAC	2028	Q/	3049	ACGGGCTTTTACCGCGGATTTTCGACTCAGTGTATCGACTGCAATCATGTGTCAACCCAGACA	3108
D/	1981	TATCATGGTGGCGGTCAAAGACCTTTGCGGCGCAAAAGGCGCCCAATCACCCAAATGTAC	2040	D/	3061	ACGGGCTTTTACCGCGGATTTTCGACTCAGTGTATCGACTGCAATCATGTGTCAACCCAGACA	3120
Q/	2029	ACCAATGTGGACAGGACCTCGTGGCTGGCAAGCGCCCCCGGGGCGCGTTCCTTGACA	2088	Q/	3109	GTGCACTTCAGCTCGGACCCGACCTTCAACATTCAGACGACGCGTSCCAACAGACGCG	3168
D/	2041	ACCAATGTGGACAGGACCTCGTGGCTGGCAAGCGCCCCCGGGGCGCGTTCCTTGACA	2100	D/	3121	GTGCACTTCAGCTCGGACCCGACCTTCAACATTCAGACGACGCGTSCCAACAGACGCG	3180
Q/	2089	CCATGCACTTCGCGGAGCTCGGACCTTTTACCTGTGTACAGAGGCATGCCGATGTCAATCCG	2148	Q/	3169	GTGTCACGCTCGCAGCGGAGGAGGACGACTGCTAGGAGGAGGATGGGCAATTTACAGTTT	3228
D/	2101	CCATGCACTTCGCGGAGCTCGGACCTTTTACCTGTGTGTACAGAGGCATGCCGATGTCAATCCG	2160	D/	3181	GTGTCACGCTCGCAGCGGAGGAGGAGGACGACTGCTAGGAGGAGGATGGGCAATTTACAGTTT	3240
Q/	2149	GTGCGCGGCGGGGCGACAGCAGGGGAGCCTACTCTCCCGAGGCGCGTCTCTACTTTG	2208	Q/	3229	GTGCACTTCAGAGAGAACCGGCCCTCGGGCATGTTCCATTTCTCGGTTCTGTGCGAGTGTAT	3288
D/	2161	GTGCGCGGCGGGGCGACAGCAGGGGAGCCTACTCTCCCGAGGCGCGTCTCTACTTTG	2220	D/	3241	GTGCACTTCAGAGAGAACCGGCCCTCGGGCATGTTCCATTTCTCGGTTCTGTGCGAGTGTAT	3300
Q/	2209	AAGGGCTCTTGGGCGGTCCACTGCTCTGCCCCCTCGGGGACGCTGTGGGCAATCTTTGCG	2268	Q/	3289	GACCGGGCTGTGTTGGTACGAGCTCAACGCGCCGAGACCTCAGTTAGGTTTCGGGCT	3348
D/	2221	AAGGGCTCTTGGGCGGTCCACTGCTCTGCCCCCTCGGGGACGCTGTGGGCAATCTTTGCG	2280	D/	3301	GACCGGGCTGTGTTGGTACGAGCTCAACGCGCCGAGACCTCAGTTAGGTTTCGGGCT	3360
Q/	2269	GCTGCCGTGTGACCCGAGGGGTTTGGAAAGCGGTGGACTTTGTACCCGCTCGAGTCTATG	2328	Q/	3349	TACCTAAACACACAGGGTTGCCCGTCTGCCAGGACCATCTGGAGTTCTTGGGAGGCGTC	3408
D/	2281	GCTGCCGTGTGACCCGAGGGGTTTGGAAAGCGGTGGACTTTGTACCCGCTCGAGTCTATG	2340	D/	3361	TACCTAAACACACAGGGTTGCCCGTCTGCCAGGACCATCTGGAGTTCTTGGGAGGCGTC	3420
Q/	2329	GAACCACTATGCGGTCCCGGTCTTCAACGCAAACTCGTCCCTCGGGCGGTACCGCAG	2388	Q/	3409	TTTACAGGCTTACCCACATAGACGCCCATTTCTTTGTCCAGACTAAGCAGGCGAGGAGAC	3468
D/	2341	GAACCACTATGCGGTCCCGGTCTTCAACGCAAACTCGTCCCTCGGGCGGTACCGCAG	2400	D/	3421	TTTACAGGCTTACCCACATAGACGCCCATTTCTTTGTCCAGACTAAGCAGGCGAGGAGAC	3480
Q/	2389	ACATTCAGGTGGCCATCTACAGCCCTCTAGTGGTAGCGACAGCATTAAGGTGCGG	2448	Q/	3469	AATTCCTCCCTACCTGTGTAGCATACAGGCTACGCTGTGCGCCAGGCTCAGGCTCCACCT	3528
D/	2401	ACATTCAGGTGGCCATCTACAGCCCTCTAGTGGTAGCGACAGCATTAAGGTGCGG	2460	D/	3481	AATTCCTCCCTACCTGTGTAGCATACAGGCTACGCTGTGCGCCAGGCTCAGGCTCCACCT	3540
Q/	2449	GCTCGGTATGACGCCCAAGGGTATAAGGTGCTTCTCTGTAACCCGCTCGCTCGCGCCACC	2508	Q/	3529	CCATCGTGGGACCAATATGTGGAAGTGTCTCATACGGCTAAGCCTACGCTGCACGGGCA	3588
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DB	3061	ACGGGCTTTACCGGGAATTTTCAGACTCAGTGATCGACTGCAATACATGTCTCAACCCAGACA	3120	DB	4141	ACCACCCAAACATACCTCTCTGTTTAAACATCTCTGGGGGATGGTGGCCGCCCAACTTGCT	4200
QY	3109	GTGCACTTCAGCTGACCGGACCTTTACCAATGTAGAGACGACCGTGCCACAAGACGGG	3168	QY	4189	CCTCCAGCGCTGCTTCTGCTTTTCGTAGCGCGCGCATCGCTGGAGCGGCTGTGTGGCAGC	4248
DB	3121	GTGCACTTCAGCTGACCGGACCTTTACCAATGTAGAGACGACCGTGCCACAAGACGGG	3180	DB	4201	CCTCCAGCGCTGCTTCTGCTTTTCGTAGCGCGCGCATCGCTGGAGCGGCTGTGTGGCAGC	4260
QY	3169	GTGTCACTGAGCGGCGAGCGAGGACTGTGTAGGGGAGGATGGGCAATTTACAGGTTT	3228	QY	4249	ATAGGCTTGGGAAGGTGCTTGTGATATTTTGGCAGGTTATGGAGCAGGGTGGCAGCG	4308
DB	3181	GTGTCACTGAGCGGCGAGCGAGGACTGTGTAGGGGAGGATGGGCAATTTACAGGTTT	3240	DB	4261	ATAGGCTTGGGAAGGTGCTTGTGATATTTTGGCAGGTTATGGAGCAGGGTGGCAGCG	4320
QY	3229	GTGACTTCAGAGGAACGGGCGCTCGGCGATGTTTCGATTCTCGTTCGTGCGAGTGCTAT	3288	QY	4309	GGGCTCGTGGCTTTTAAAGGTATGAGCGCGAGATGCGCTCCACCGAGACCTGGGTAAC	4368
DB	3241	GTGACTTCAGAGGAACGGGCGCTCGGCGATGTTTCGATTCTCGTTCGTGCGAGTGCTAT	3300	DB	4321	GGGCTCGTGGCTTTTAAAGGTATGAGCGCGAGATGCGCTCCACCGAGACCTGGTAAAC	4380
QY	3289	GACGGGGCTGTGCTGT	3348	QY	4369	CTACTCCCTGTCTATCTCTCCCTGGCGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	4428
DB	3301	GACGGGGCTGTGCTGT	3360	DB	4381	CTACTCCCTGTCTATCTCTCCCTGGCGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	4440
QY	3349	TACCTTAACACACAGGCTGTGCGGCTGTGCGAGGACCTGTGGAGTTCTGGAGAGCGTC	3408	QY	4429	CTGCGTCCGACAGTGGGCGGAGGGGCTGTGAGTGTGATGATGATGATGATGATGATGATGATG	4488
DB	3361	TACCTTAACACACAGGCTGTGCGGCTGTGCGAGGACCTGTGGAGTTCTGGAGAGCGTC	3420	DB	4441	CTGCGTCCGACAGTGGGCGGAGGGGCTGTGAGTGTGATGATGATGATGATGATGATGATGATG	4500
QY	3409	TTTACAGGCTCACCCACATAGACGCCATTTCTGTCCAGACTAAGCAGGACGAGAC	3468	QY	4489	TTTCGCTTCGCGGGTAAACACAGCTCTCCCGCACACTATGTCTGAGAGCAGCGTCA	4548
DB	3421	TTTACAGGCTCACCCACATAGACGCCATTTCTGTCCAGACTAAGCAGGACGAGAC	3480	DB	4501	TTTCGCTTCGCGGGTAAACACAGCTCTCCCGCACACTATGTCTGAGAGCAGCGTCA	4560
QY	3469	AACTTCCCTACTCTGT	3528	QY	4549	GCAGTGTCACTCAGATCCTCTCTAGTCTTACCATCACTCACTCACTCACTCACTCACTCACT	4608
DB	3481	AACTTCCCTACTCTGT	3540	DB	4561	GCAGTGTCACTCAGATCCTCTCTAGTCTTACCATCACTCACTCACTCACTCACTCACTCACT	4620
QY	3529	CCATGTGGGACCAATGTGGAGTGTCTCATACGGCTTAAGCTTACGCTGTGACGGGCA	3588	QY	4609	CAGTGGATCAAGAGGATGTCTCCAGCGCATCTCGGCTCGTGGCTTAAGAGATGTTGG	4668
DB	3541	CCATGTGGGACCAATGTGGAGTGTCTCATACGGCTTAAGCTTACGCTGTGACGGGCA	3600	DB	4621	CAGTGGATCAAGAGGATGTCTCCAGCGCATCTCGGCTCGTGGCTTAAGAGATGTTGG	4680
QY	3589	ACGCCCTCTCTGTATAGGCTGGGAGCGGTTCAAAACGAGGTACTACACACACGCCATA	3648	QY	4669	GATTGGATGACAGGCTGTGACTGATTTCAAGACTGGCTCCAGTCCAGTCCCTGCCG	4728
DB	3601	ACGCCCTCTCTGTATAGGCTGGGAGCGGTTCAAAACGAGGTACTACACACACGCCATA	3660	DB	4681	GATTGGATGACAGGCTGTGACTGATTTCAAGACTGGCTCCAGTCCAGTCCCTGCCG	4740
QY	3649	ACCAATACATCATGGCATGTGCGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT	3708	QY	4729	CGATTCCGGGAGTCCCTTCTCTCATGTCAACGTGGGTACAAGGAGTCTGGGGGGC	4788
DB	3661	ACCAATACATCATGGCATGTGCGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT	3720	DB	4741	CGATTCCGGGAGTCCCTTCTCTCATGTCAACGTGGGTACAAGGAGTCTGGGGGGC	4800
QY	3709	CTGGTAGGAGTCTTAGCAGCTGTGGCGGTATTGCTGTGCTGTGCTGTGCTGTGCTGTGCT	3768	QY	4789	GACGCACTATCATCAACACCTGCGCATGTGGAGCACAGATCACCGGATCTGAAAAA	4848
DB	3721	CTGGTAGGAGTCTTAGCAGCTGTGGCGGTATTGCTGTGCTGTGCTGTGCTGTGCTGTGCT	3780	DB	4801	GACGCACTATCATCAACACCTGCGCATGTGGAGCACAGATCACCGGATCTGAAAAA	4860
QY	3769	ATTGTGGGAGGATCATCTTGTCCGGAAGCGCGGCATCATTTCCCGACAGGAGTCTCTT	3828	QY	4849	GGTTCCATGAGGATCGTGGGGCTTAGGACCTGTAGTAAACACGTGGCATGGAACATTTCCCG	4908
DB	3781	ATTGTGGGAGGATCATCTTGTCCGGAAGCGCGGCATCATTTCCCGACAGGAGTCTCTT	3840	DB	4861	GGTTCCATGAGGATCGTGGGGCTTAGGACCTGTAGTAAACACGTGGCATGGAACATTTCCCG	4920
QY	3829	TACCGGAGTTCGATGAGATGAAGTGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT	3888	QY	4909	ATTAAAGGATACACACGGGCGGCTGTGACGCGCTCCCGCGCGCCAAAATTATTCTAGGGCG	4968
DB	3841	TACCGGAGTTCGATGAGATGAAGTGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT	3900	DB	4921	ATTAAAGGATACACACGGGCGGCTGTGACGCGCTCCCGCGCGCCAAAATTATTCTAGGGCG	4980
QY	3889	ATGCACTCGCGGACCAATTCACACAGAGGCAATCGGGTTCGCTGCAACAGCCACCAAG	3948	QY	4969	CTGTCGCGGTGCTGTGAGGATGACGTGGAGGTTACGCGGTGGGGATTTCCACATAC	5028
DB	3901	ATGCACTCGCGGACCAATTCACACAGAGGCAATCGGGTTCGCTGCAACAGCCACCAAG	3960	DB	4981	CTGTCGCGGTGCTGTGAGGATGACGTGGAGGTTACGCGGTGGGGATTTCCACATAC	5040
QY	3949	CAAGCGGAGGCTGTGCTCCCGTGTGGAAATCAAGTGGCGGACCGCTCGAAGCCTTCTGG	4008	QY	5029	GTGACGGGATGACCACTGACAAAGTGGCGCTGTGAGTTCGCGGCTCCCGCGCGGAAATTC	5088
DB	3961	CAAGCGGAGGCTGTGCTCCCGTGTGGAAATCAAGTGGCGGACCGCTCGAAGCCTTCTGG	4020	DB	5041	GTGACGGGATGACCACTGACAAAGTGGCGCTGTGAGTTCGCGGCTCCCGCGCGGAAATTC	5100
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QY	4069	CTGGCAACCCCGGATAGCATCTGATGGATTTACAGGCTCTATACACAGCGCGCTC	4128	QY	5149	CGGAGGAGGTACATCTCTGCTGGGCTCAATCAATACCTGTTGGGTTCACAGCTCCCA	5208
DB	4081	CTGGCAACCCCGGATAGCATCTGATGGATTTACAGGCTCTATACACAGCGCGCTC	4140	DB	5161	CGGAGGAGGTACATCTCTGCTGGGCTCAATCAATACCTGTTGGGTTCACAGCTCCCA	5220
				QY	5209	TGCGAGCCGGAACCGGACGTAGAGTGTCTCACTTCAATGTCTACCGAACCCCTCCCACTT	5268

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VERSION AX036259.1 GI:11225875
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ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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1 Bartschschlager,R.D.
AUTHORS Hepatitis C virus cell culture system
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RESULT 10
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ACCESSION AR406045
VERSION AR406045.1 GI:40155172
KEYWORDS
SOURCE Unknown.
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AX036257
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DEFINITION Sequence 6 from Patent EP1043399.
ACCESSION AX036257
VERSION AX036257.1 GI:11225873
KEYWORDS
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
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1. Bartschlag, R.D.
AUTHORS Bartschlag, R.D.
TITLE Hepatitis C virus cell culture system
JOURNAL Patent: EP 1043399-A 6 11-OCT-2000;
BARTENSCHLAGER RALF DR (DE)
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Db 1081 TTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCTCTGCTTACGGTATCGCCG 1140
QY 1129 CTCGCGATTGCGAGCGCATCGCTTCTATCGGCTTCTTACGAGTTCCTCTGAGTTTAA 1188
Db 1141 CTCGCGATTGCGAGCGCATCGCTTCTATCGGCTTCTTACGAGTTCCTCTGAGTTTAA 1200
QY 1189 CAGACCAACCGTTCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCT 1248
Db 1201 CAGACCAACCGTTCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCT 1260
QY 1249 AACGTTACTTGGCGAAGCGCTTGGAAATAGGCGCGGTGCGCTTCTCTATATGTTATT 1308
Db 1261 AACGTTACTTGGCGAAGCGCTTGGAAATAGGCGCGGTGCGCTTCTCTATATGTTATT 1320
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Db 1441 GTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGCAACCAACAGTCTCTAGCGACCTT 1500
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QY 4669 GATTGGATATGACGCTGTGACTGATTTCAAGACCTGGCTCAAGTCCAGCTCTCCGCG 4728
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Db	6181	CACTACCGGGACGTGCTCAAGGAGATGAAGGGAAAGGGCGTCACAGTTAAAGGCTAAACTTT	6240
QY	6229	CTATCGTGTGAGGAAGCTGTGAAGCTGACGCCCCACATTTCCGCCAGATCTTAAATTGGC	6288
Db	6241	CTATCGTGTGAGGAAGCTGTGAAGCTGACGCCCCACATTTCCGCCAGATCTTAAATTGGC	6300
QY	6289	TATGGGGCAAAAGACCTGCGGAACCTTATCCAGCAAGGCGGTTAAACACATCCGCTCCGGTG	6348
Db	6301	TATGGGGCAAAAGACCTGCGGAACCTTATCCAGCAAGGCGGTTAAACACATCCGCTCCGGTG	6360
QY	6349	TGGAAGGACTTGTCTGGAAGACACTGAGACACCAATTGACACCAACCATCATATGCGAAATAAT	6408
Db	6361	TGGAAGGACTTGTCTGGAAGACACTGAGACACCAATTGACACCAACCATCATATGCGAAATAAT	6420
QY	6409	GAGGTTTTCTGCGTCCAAACAGAGAGAGGGGGCGCAAGCCAGCTCGCCTTATCGTATTTC	6468
Db	6421	GAGGTTTTCTGCGTCCAAACAGAGAGAGGGGGCGCAAGCCAGCTCGCCTTATCGTATTTC	6488
QY	6469	CCAGATTTGGGGGTTTCGTGTGTCGGAGAAAATGGCGCTTTACGATGTGCTCTCCACCCCTC	6528
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QY	6529	CCTCAGGCCGTGATGGGCTCTTCATACGGATTCCAATATCTCTCTGGACAGCGGGTCGAG	6588
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QY	6769	GGGGCCCCCTGACTAATTTCTAAGGGCAGAACTGGGGCTATCGCGGTGCGCCGCGGAGC	6828
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QY	6889	TGTCGAGCTCGAAGCTCCAGGACTGCAAGATGCTCGTATGCGGAGACGACCTTGTGCTT	6948
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QY	6949	ATCTGTAAAGCGGGGAGCCCAAGAGGACGAGCGAGCCTACGGGCTTTCACGGAGGCT	7008
Db	6961	ATCTGTAAAGCGGGGAGCCCAAGAGGACGAGCGAGCCTACGGGCTTTCACGGAGGCT	7020
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Db	7021	ATGACTAGATACTCTGCCCCCTTGGGGACCGGCCCAAACAGAAATACGACTTTGGAGTTG	7080
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Db	7141	TATCTCACCGGTGACCCGACACACCCCTTTCGCGGGGCTGGTGGGAGACAGCTAGACAC	7200
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QY	7849	TT	TTCTCCTTTTTTTTTTTCCTTTTTTTTTTCTTT	7908		
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RESULT 13						
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 QY 1261 CGAAGCGCTTGAATAAGGCGGCTGTGCTTGTCTATATGTTATTTCCACCATATG 1320
 Db 1261 CGAAGCGCTTGAATAAGGCGGCTGTGCTTGTCTATATGTTATTTCCACCATATG 1320
 QY 1321 CCGTCTTTGGCAATGTGAGGCGCGGAAACCTGGCCCTCTCTTTGACGAGCATTCCT 1380
 Db 1321 CCGTCTTTGGCAATGTGAGGCGCGGAAACCTGGCCCTCTCTTTGACGAGCATTCCT 1380
 QY 1381 AGGGCTTCTTCCCTCTCGCCAAAGGAATGCAAGGCTGTGTTGAAATGCTGGAAGGA 1440
 Db 1381 AGGGCTTCTTCCCTCTCGCCAAAGGAATGCAAGGCTGTGTTGAAATGCTGGAAGGA 1440
 QY 1441 GTTCTCTGGAAGCTTCTTGAAGCAAAACAGCTGTGAGGACCTTTGACGAGCGG 1500
 Db 1441 GTTCTCTGGAAGCTTCTTGAAGCAAAACAGCTGTGAGGACCTTTGACGAGCGG 1500
 QY 1501 AACCCCGCATCTGGCGAGCTGCTCTGCGGCAAAAGCCAGCTGATATAGATACACT 1560
 Db 1501 AACCCCGCATCTGGCGAGCTGCTCTGCGGCAAAAGCCAGCTGATATAGATACACT 1560
 QY 1561 GCAAGGCGCACACCCAGTGGCCAGCTTGTGAGTTGGATGTTGTGGAAGAGTCAAA 1620
 Db 1561 GCAAGGCGCACACCCAGTGGCCAGCTTGTGAGTTGGATGTTGTGGAAGAGTCAAA 1620
 QY 1621 TGGCTCTCTCAAGGATTTCAAAGGGCTGAGGATGCCAGAGGTACCCCATTTG 1680
 Db 1621 TGGCTCTCTCAAGGATTTCAAAGGGCTGAGGATGCCAGAGGTACCCCATTTG 1680
 QY 1681 ATGGGATCTGATCTGGGCGCTCGGTGCACTGCTTTACATGTTGTTAGTCGAGTTAAAA 1740

Db 1681 ATGGGATCTGATCTGGGCGCTCGGTGCACATGCTTTACATGTTTGTAGTCAGGTTAAAA 1740
 QY 1741 AAGTCTAGGCGCCCGGAAACACGCGGACGCTGTTTCTTTGAAAAACGATATATACC 1800
 Db 1741 AAGTCTAGGCGCCCGGAAACACGCGGACGCTGTTTCTTTGAAAAACGATATATACC 1800
 QY 1801 ATG----- 1803
 Db 1801 ATGACCGGAGATGGCAGCATCTGCGGAGCGCGGTTTTCTGTAGTCTGATATCTTTG 1860
 QY 1804----- 1803
 Db 1861 ACCTTGTACCGCATATAAGCTGTTCTGCTAGGCTCATATGTTGTTTACATATTTT 1920
 QY 1804----- 1803
 Db 1921 ATCACCAGGCGGAGGACACCTTGCAGTGTGATCCCCCCTCAACGTTCCGGGGGCG 1980
 QY 1804----- 1803
 Db 1981 CGCGATCGGTCATCTCTCTCAGTGTGCGGATCCACCAGAGCTAATCTTTACATCACC 2040
 QY 1804----- 1803
 Db 2041 AAAATCTTGTGCGCATACTCGTCCACTCATGTGTCTCCAGGCTGTTATTAACCAAGTG 2100
 QY 1804----- 1803
 Db 2101 CCGTACTTGTGCGGACACCGGGCTCATTCGTGATGATGCTGTGTGCGAAGTTGCT 2160
 QY 1804----- 1803
 Db 2161 GGSGGTCAATTATGTCCAAATGGCTCTCATGAAATTTGGCGCACTGACAGGTACGTACGTT 2220
 QY 1804----- 1803
 Db 2221 TATGACCATCTCACCCACTGCGGAGCTGGGCCACCGGGCTTACAGACCTTTCGGTG 2280
 QY 1804----- 1803
 Db 2281 GCAGTTGAGCCGCTGCTTCTCTGATATGAGACCAAGTTATCACCTGGGGGCGAGAC 2340
 QY 1804----- 1803
 Db 2341 ACCGCGCGTGTGGGACATCATCTTGGGCTCCCGCTCTCCGCGCGCGGGGAGGAG 2400
 QY 1804----- 1812
 Db 2401 ATACATCTGGGACCGGCGAGACGCTTGAAGGCGAGGGTGGCGACTCTCTCGCGCTATT 2460
 QY 1813 ACCGCTTACTCCCAACAGACGCGAGGCTTACTTGGGTGATCATCATCTAGCTCACAGGC 1872
 Db 2461 ACCGCTTACTCCCAACAGACGCGAGGCTTACTTGGGTGATCATCATCTAGCTCACAGGC 2520
 QY 1873 CGGACAGGAACAGGTCGAGGGGAGGTCAGGTGCTCTCCCGCAACACATCTTTC 1932
 Db 2521 CGGACAGGAACAGGTCGAGGGGAGGTCAGGTGCTCTCCCGCAACACATCTTTC 2580
 QY 1933 CTGGGACCTTGGCTCAATGCGTGTGTTGACTCTCTATCATGTGCGGCTCAAGAC 1992
 Db 2581 CTGGGACCTTGGCTCAATGCGTGTGTTGACTCTCTATCATGTGCGGCTCAAGAC 2640
 QY 1993 CTTTCCCGCCCAAGGGCCCAATCAACCAATGTACCAATGTGACCAATGTGACCAAGCTGTC 2700
 Db 2641 CTTTCCCGCCCAAGGGCCCAATCAACCAATGTACCAATGTGACCAAGCTGTC 2700
 QY 2053 GGTGCGCAAGCGCCCGCGGCGGTTCTTTGACCATCATCTGCTGGAGCTCGGAC 2112
 Db 2701 GGTGCGCAAGCGCCCGCGGCGGTTCTTTGACCATCATCTGCTGGAGCTCGGAC 2760
 QY 2113 CTTTACTTGGTCAAGGACATCGGATGTCATTCGGTGGCGCGGCGGCGGACAGG 2172

Db	2761	CTTTACTTGGTCACGAGGATGCCGATGTCATTTCCGGTGGCGGCGGCGACACAGG	2820
QY	2173	GGAGAGCTACTCTCCCGACGGCCGTCCTCTACTTGAAGGCTCTTTCGGCGCGTCCACTG	2232
Db	2821	GGAGAGCTACTCTCCCGACGGCCGTCCTCTACTTGAAGGCTCTTTCGGCGCGTCCACTG	2880
QY	2233	CTCTGCCCTCGGGGACGCTGTGGGCACTCTTTCGGGCTGCCGTGTGCAACCGAGGGGTT	2292
Db	2881	CTCTGCCCTCGGGGACGCTGTGGGCACTCTTTCGGGCTGCCGTGTGCAACCGAGGGGTT	2940
QY	2293	GGAAAGGCGGTGGACTTTGTACCCGTCGAGTCTATGGAAACCACTATGCGGTCCCGGTC	2352
Db	2941	GGAAAGGCGGTGGACTTTGTACCCGTCGAGTCTATGGAAACCACTATGCGGTCCCGGTC	3000
QY	2353	TTACGGCAAACTCTGCCCTCGGCGGTACCGCAGACATTCACAGTGGCCCACTACAC	2412
Db	3001	TTACGGCAAACTCTGCCCTCGGCGGTACCGCAGACATTCACAGTGGCCCACTACAC	3060
QY	2413	GCCCTACTGTAGCGGCAAGAGCACTAAGGTGCCGTGGGTATGCAAGCCCAAGGGTAT	2472
Db	3061	GCCCTACTGTAGCGGCAAGAGCACTAAGGTGCCGTGGGTATGCAAGCCCAAGGGTAT	3120
QY	2473	AAGGTGCTTGTCTTGAACCCGTCGCTCGCGCCGCACTAGGTTTCGGGCGGTATATGTC	2532
Db	3121	AAGGTGCTTGTCTTGAACCCGTCGCTCGCGCCGCACTAGGTTTCGGGCGGTATATGTC	3180
QY	2533	AAGGCATGTGTATGACCCCTAACATCAGAACCGGGGTAAAGCACTCACCACGGGTGCC	2592
Db	3181	AAGGCATGTGTATGACCCCTAACATCAGAACCGGGGTAAAGCACTCACCACGGGTGCC	3240
QY	2593	CCCATCAGTACTCAGCTATGGCAAGTCTTCTGCGAGCGGTGTGCTGCGGCGGCC	2652
Db	3241	CCCATCAGTACTCAGCTATGGCAAGTCTTCTGCGAGCGGTGTGCTGCGGCGGCC	3300
QY	2653	TATGACATCATATATGTATGATGAGTGCACCTCAACTGACTCGACCATCTCCTGGGATC	2712
Db	3301	TATGACATCATATATGTATGATGAGTGCACCTCAACTGACTCGACCATCTCCTGGGATC	3360
QY	2713	GGCAGCTCTGGACCAAGCGGAGACGGCTGGAGCGGACTCGTCTGCTCGCCACCGCT	2772
Db	3361	GGCAGCTCTGGACCAAGCGGAGACGGCTGGAGCGGACTCGTCTGCTCGCCACCGCT	3420
QY	2773	ACGCTCTCGGGATCGGTACCGTGCACATCCAAATCGAGAGGTGGCTGTCTCCAGC	2832
Db	3421	ACGCTCTCGGGATCGGTACCGTGCACATCCAAATCGAGAGGTGGCTGTCTCCAGC	3480
QY	2833	ACTGGAGAAATCCCTTTTATGGCAAGCCATCCCATCGAGACCATCAAGGGGGGAGG	2892
Db	3481	ACTGGAGAAATCCCTTTTATGGCAAGCCATCCCATCGAGACCATCAAGGGGGGAGG	3540
QY	2893	CACCTCATTTCTGCGCATTCAGAGAAATGTGATGAGCTCGCGCGAAGCTGTCCGCG	2952
Db	3541	CACCTCATTTCTGCGCATTCAGAGAAATGTGATGAGCTCGCGCGAAGCTGTCCGCG	3600
QY	2953	CTCGGACTCAATGCTGTAGCATATACCGGGGCTTGATGTATCGTGTATACCACTAGC	3012
Db	3601	CTCGGACTCAATGCTGTAGCATATATACCGGGGCTTGATGTATCGTGTATACCACTAGC	3660
QY	3013	GGAGAGCTCATTTGCTGTAGCAACGAGCGCTCTAATGACGGGCTTTACCGGCAATTCGAC	3072
Db	3661	GGAGAGCTCATTTGCTGTAGCAACGAGCGCTCTAATGACGGGCTTTACCGGCAATTCGAC	3720
QY	3073	TCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	3132
Db	3721	TCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	3780
QY	3133	TTACCATTTGAGACGACCGTGCACAGAGCGGGTGTACGCTCGAGCGCGAGGC	3192
Db	3781	TTACCATTTGAGACGACCGTGCACAGAGCGGGTGTACGCTCGAGCGCGAGGC	3840
QY	3193	AGGACTGTAGGGGAGGATGGGATTTTACAGTTTGTGACTCCAGAGAACGGCCCTCG	3252
Db	3841	AGGACTGTAGGGGAGGATGGGATTTTACAGTTTGTGACTCCAGAGAACGGCCCTCG	3900
QY	3253	GGCATGTTCCATTTCTCTCGGTTCTGTGCGAGTGTATGACGCGGCGTGTCTTGGTAGAG	3312
Db	3901	GGCATGTTCCATTTCTCTCGGTTCTGTGCGAGTGTATGACGCGGCGTGTCTTGGTAGAG	3960
QY	3313	CTACGCGCGCGGAGACCTCACTTGGTTCGGGCTTACCTAAACACACACCGGTTGCC	3372
Db	3961	CTACGCGCGCGGAGACCTCACTTGGTTCGGGCTTACCTAAACACACACCGGTTGCC	4020
QY	3373	GTCTGCCAGGACCATCTCTGGAGTCTTGGAGAGCGCTTTTACAGGCTTACCCATAGAC	3432
Db	4021	GTCTGCCAGGACCATCTCTGGAGTCTTGGAGAGCGCTTTTACAGGCTTACCCATAGAC	4080
QY	3433	GCCCATTTCTGTCCAGACTAAGCAGGAGAGAGCACTTCCCTTACCTGTAGCATAC	3492
Db	4081	GCCCATTTCTGTCCAGACTAAGCAGGAGAGAGCACTTCCCTTACCTGTAGCATAC	4140
QY	3493	CAGGCTAGGTTGGCGGCGAGGCTCAGGCTCCACCTCCATCGTGGGACCAATGTGGAAG	3552
Db	4141	CAGGCTAGGTTGGCGGCGAGGCTCAGGCTCCACCTCCATCGTGGGACCAATGTGGAAG	4200
QY	3553	TGTCTCATACCGCTAAAGCCCTACGCTGACGCGGCAACGCGCTGTGTATAGGCTGGA	3612
Db	4201	TGTCTCATACCGCTAAAGCCCTACGCTGACGCGGCAACGCGCTGTGTATAGGCTGGA	4260
QY	3613	GCCGTTCAAAACGAGGTTACTTACACACACCCCATACCAATATACATGCGCATGATG	3672
Db	4261	GCCGTTCAAAACGAGGTTACTTACACACACCCCATACCAATATACATGCGCATGATG	4320
QY	3673	TCGCTCAGCTGGAGTTCGTACGAGCACTGGGTGTGTGTAGGCGGAGTCTTAGCAGCT	3732
Db	4321	TCGCTCAGCTGGAGTTCGTACGAGCACTGGGTGTGTGTAGGCGGAGTCTTAGCAGCT	4380
QY	3733	CTGCGCGCTATTGCTGCAACAGGCGAGCTGTGCTTACCGGGAGTTCGATGAGATGGA	3792
Db	4381	CTGCGCGCTATTGCTGCAACAGGCGAGCTGTGCTTACCGGGAGTTCGATGAGATGGA	4440
QY	3793	GGAGGCGCGCATCATTTCCCGACAGGAACTCTTTTACCGGGAGTTCGATGAGATGGA	3852
Db	4441	GGAGGCGCGCATCATTTCCCGACAGGAACTCTTTTACCGGGAGTTCGATGAGATGGA	4500
QY	3853	GAGTGGCGCTCACACCTCCCTTACATCGAACAGGAAATGAGTTCGCGCAACATTCAAA	3912
Db	4501	GAGTGGCGCTCACACCTCCCTTACATCGAACAGGAAATGAGTTCGCGCAACATTCAAA	4560
QY	3913	CAGAGGCAATCGGGTTGCTGCAACAGCCACCAAGCGAGCTGTGCTGCTCCGCTG	3972
Db	4561	CAGAGGCAATCGGGTTGCTGCAACAGCCACCAAGCGAGCTGTGCTGCTCCGCTG	4620
QY	3973	GTGGAATCCAGTGGCGGACCTTCGAAAGCTTTCTGGGCGAAGCATATGTGGAATTCATC	4032
Db	4621	GTGGAATCCAGTGGCGGACCTTCGAAAGCTTTCTGGGCGAAGCATATGTGGAATTCATC	4680
QY	4033	AGCGGATACATATTTAGCAGCTTGTCCATCTGCTGTGGCAACCCCGCATAGCATCA	4092
Db	4681	AGCGGATACATATTTAGCAGCTTGTCCATCTGCTGTGGCAACCCCGCATAGCATCA	4740
QY	4093	CTGATGGCATTCACAGCTCTATCACAGCGCTTATCACAGCGCTTATCACAGCGCTTAT	4152
Db	4741	CTGATGGCATTCACAGCTCTATCACAGCGCTTATCACAGCGCTTATCACAGCGCTTAT	4800
QY	4153	AACATCTGGGGGATGGGTGGCGCCCAACTTGTCTCTCCAGCGCTGTCTTCTGCTTTC	4212
Db	4801	AACATCTGGGGGATGGGTGGCGCCCAACTTGTCTCTCCAGCGCTGTCTTCTGCTTTC	4860
QY	4213	GTAGCGCGCATCTGAGAGCGGCTTGTGGAGCATAGGCTTGGAGAGGTGCTTGTG	4272
Db	4861	GTAGCGCGCATCTGAGAGCGGCTTGTGGAGCATAGGCTTGGAGAGGTGCTTGTG	4920
QY	4273	GATATTTTGGCAGGTTATGGAGAGGCTGTGCGAGCGCTTGTGGAGAGGTGCTTGTG	4332
Db	4921	GATATTTTGGCAGGTTATGGAGAGGCTGTGCGAGCGCTTGTGGAGAGGTGCTTGTG	4980

QY	4333	AGCGGAGATGCTCCACCGAGGACCTGGCTAACTCTCCTGCTATCCTCTCCCT	Db	6061	AACCTCTGTGGCGGAGAGATGGCGGGAACATCACCGCGTGGAGTCAGAAATAAG	6120
Db	4981	AGCGGAGATGCTCCACCGAGGACCTGTTAACTCTCCTGCTATCCTCTCCCT	QY	5473	GTAGTAATTTTGGACTCTTTTCGAGCGCTCCAAAGCGGAGGAGATGAGAGGAGTATCC	5532
QY	4393	GGCGGCTAGTGTGCGGGGTGCTGCGGAGGATAGTGGTGGGCGGCGGCGG	Db	6121	GTAGTAATTTTGGACTCTTTTCGAGCGCTCCAAAGCGGAGGAGATGAGAGGAGTATCC	6180
Db	5041	GGCGGCTAGTGTGCGGGGTGCTGCGGAGGATAGTGGTGGGCGGCGGCGG	QY	5533	GTTCGCGGAGATCTTCGCGGAGTCCAGAAATTCCTCGAGGATGCCATATGGCA	5592
QY	4453	GAGGGCTGTGAGTGAGTGAACCGGCTGATAGCTTTCGCGGGGTAAACAGTC	Db	6181	GTTCGCGGAGATCTTCGCGGAGTCCAGAAATTCCTCGAGGATGCCATATGGCA	6240
Db	5101	GAGGGCTGTGAGTGAGTGAACCGGCTGATAGCTTTCGCGGGGTAAACAGTC	QY	5593	CGCGCGGATTAACACCTCCACTGTAGAGTCTCGGAGGACCGGAGTACCTCCCTCCA	5652
QY	4513	TCCCGGAGCTATGCTGAGAGGAGCGCTGAGAGCTGTACATCAGATCTCTCT	Db	6241	CGCGCGGATTAACACCTCCACTGTAGAGTCTCGGAGGACCGGAGTACCTCCCTCCA	6300
Db	5161	TCCCGGAGCTATGCTGAGAGGAGCGCTGAGAGCTGTACATCAGATCTCTCT	QY	5653	GTGTATACCGGCTGTCCATTCGCGCTCCAAAGCGCTCCGATACCACTCCACGAGG	5712
QY	4573	AGTCTTACATCTAGCTGCTGAGAGGCTTCAACAGTGATCAACGAGGACTGTCC	Db	6301	GTGTATACCGGCTGTCCATTCGCGCTCCAAAGCGCTCCGATACCACTCCACGAGG	6360
Db	5221	AGTCTTACATCTAGCTGCTGAGAGGCTTCAACAGTGATCAACGAGGACTGTCC	QY	5713	AAGAGGAGGCTGTCTCTGTCAGAAATCTACCTGTCTTCTGCTTGGCGGAGTCCGCA	5772
QY	4633	ACGCGATCTCCGGCTGCTGAGAGGCTTCAACAGTGATCAACGAGGACTGTCC	Db	6361	AAGAGGAGGCTGTCTCTGTCAGAAATCTACCTGTCTTCTGCTTGGCGGAGTCCGCA	6420
Db	5281	AGTCTTACATCTAGCTGCTGAGAGGCTTCAACAGTGATCAACGAGGACTGTCC	QY	5773	AAGACCTTTCGCGAGCTCCGAAATCTGCGCGCTCGACAGCGCAACCGGCTCTCT	5832
QY	4693	GATTTCAAGAGCTGGCTCCAGTCCAAAGTCTGCGCGGATTCGCGGGAGTCCCTTCT	Db	6421	AAGACCTTTCGCGAGCTCCGAAATCTGCGCGCTCGACAGCGCAACCGGCTCTCT	6480
Db	5341	GATTTCAAGAGCTGGCTCCAGTCCAAAGTCTGCGCGGATTCGCGGGAGTCCCTTCT	QY	5833	GACGAGGCTTCGAGCGGAGCGCGGATCCGAGCTTGGAGTCTGCTCTCTCTCTCT	5892
QY	4753	TCATGTCAAGTGGGTACAGGAGTCTGGCGGGGAGCGGATCATGCAACACCTGC	Db	6481	GACGAGGCTTCGAGCGGAGCGCGGATCCGAGCTTGGAGTCTGCTCTCTCTCTCT	6540
Db	5401	TCATGTCAAGTGGGTACAGGAGTCTGGCGGGGAGCGGATCATGCAACACCTGC	QY	5893	CCCTTTGAGGGGAGCGCGGGGATCCCGATCTCAGCGAGCGGTCTTGGTCTACCGTAAGC	5952
QY	4813	CCATGTGAGGACAGATCACCGGACATGTGAAAACGGTTCATGAGGATCGTGGGCT	Db	6541	CCCTTTGAGGGGAGCGCGGGGATCCCGATCTCAGCGAGCGGTCTTGGTCTACCGTAAGC	6600
Db	5461	CCATGTGAGGACAGATCACCGGACATGTGAAAACGGTTCATGAGGATCGTGGGCT	QY	5953	GAGGAGGCTAGTGGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	6012
QY	4873	AGGACCTGTAGTAACAGTGGGATGGAACATTTCCCGCATTAACCGGTACACCGGCGCC	Db	6601	GAGGAGGCTAGTGGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	6660
Db	5521	AGGACCTGTAGTAACAGTGGGATGGAACATTTCCCGCATTAACCGGTACACCGGCGCC	QY	6013	ATCAGCGCATGCTGCGGAGGAAACCAAGCTGCCCATCAATGCTGAGCAACTCTTTG	6072
QY	4933	TGACCGCTTCCCGGCGCAATTAATTTAGGGCGCTGTGGCGGCTGGCTGCTGAGGAG	Db	6661	ATCAGCGCATGCTGCGGAGGAAACCAAGCTGCCCATCAATGCTGAGCAACTCTTTG	6720
Db	5581	TGACCGCTTCCCGGCGCAATTAATTTAGGGCGCTGTGGCGGCTGGCTGCTGAGGAG	QY	6073	CTCCGTCACCAACAACTTGTGTATGTACAACTCTCGGAGCGAGCTCGGCGAGAG	6132
QY	4993	TACGTGAGGATACGGGGTGGGGATTTCCACTAGTGAAGGAGTACCACTGAGCAAC	Db	6721	CTCCGTCACCAACAACTTGTGTATGTACAACTCTCGGAGCGAGCTCGGCGAGAG	6780
Db	5641	TACGTGAGGATACGGGGTGGGGATTTCCACTAGTGAAGGAGTACCACTGAGCAAC	QY	6133	AAGTTCACCTTTGACAGACTGCGAGGTCCTGGAGCGACCTACCGGAGCGTCTCAAGGAG	6192
QY	5053	GTAAAGTGGCGGTGAGGTTCCGGGCGGCGGAAATTTCTACAGAGTGGATGGGTGCGG	Db	6781	AAGTTCACCTTTGACAGACTGCGAGGTCCTGGAGCGACCTACCGGAGCGTCTCAAGGAG	6840
Db	5701	GTAAAGTGGCGGTGAGGTTCCGGGCGGCGGAAATTTCTACAGAGTGGATGGGTGCGG	QY	6193	ATGAAGCGAAGCGGTCCACAGTTAAGGCTTAACTTTCTATCCGTGGAGGAGCTGTAAAG	6252
QY	5113	TTGCAAGGTACGCTCCAGGTCGCAACCTCTTACGAGGAGGCTCACTTCTCTGCTC	Db	6841	ATGAAGCGAAGCGGTCCACAGTTAAGGCTTAACTTTCTATCCGTGGAGGAGCTGTAAAG	6300
Db	5761	TTGCAAGGTACGCTCCAGGTCGCAACCTCTTACGAGGAGGCTCACTTCTCTGCTC	QY	6253	CTGACGCGCCCAACTTCGCGGAGATTAATTTGGCTATGGGCAAGGAGCTCCGGAAC	6312
QY	5173	GGGCTCAATCAATACCTTGGGTGAGTCCAGTCCGAGGCGGAGCGGAGTACGA	Db	6901	CTGACGCGCCCAACTTCGCGGAGATTAATTTGGCTATGGGCAAGGAGCTCCGGAAC	6360
Db	5821	GGGCTCAATCAATACCTTGGGTGAGTCCAGTCCGAGGCGGAGCGGAGTACGA	QY	6313	CTATCCAGGAGCGGCTTAAACCATCCGCTCCGTGTGGAGGAGCTTGTCTGGAGACACT	6372
QY	5233	GTGCTCATCTTCATGCTACCGACCTCCACATTAACGCGGAGCGGCTAAGCGTAGG	Db	6961	CTATCCAGGAGCGGCTTAAACCATCCGCTCCGTGTGGAGGAGCTTGTCTGGAGACACT	7020
Db	5881	GTGCTCATCTTCATGCTACCGACCTCCACATTAACGCGGAGCGGCTAAGCGTAGG	QY	6373	GAGACCAATTTGACACCACTCATGCGCAAAATAAGGTTTCTCGGTCCACCGAGAG	6432
QY	5293	CTGGCGAGGAGTCTCCCGCTCTTGGCGAGCTCATCAGCTAGCGAGCTGTCTGCGGCT	Db	7021	GAGACCAATTTGACACCACTCATGCGCAAAATAAGGTTTCTCGGTCCACCGAGAG	7080
Db	5941	CTGGCGAGGAGTCTCCCGCTCTTGGCGAGCTCATCAGCTAGCGAGCTGTCTGCGGCT	QY	6433	AAGGGGCGCGCAAGCGAGCTCGCTTATCGTATTCAGATTTGGGGGTTCTGTGTGTC	6492
QY	5353	TCCCTGAAGGCAACATGACCTACCGGTCAATGATCTCCCGGAGCGTACCTCATCGAGCC	Db	7081	AAGGGGCGCGCAAGCGAGCTCGCTTATCGTATTCAGATTTGGGGGTTCTGTGTGTC	7140
Db	6001	TCCCTGAAGGCAACATGACCTACCGGTCAATGATCTCCCGGAGCGTACCTCATCGAGCC	QY	6493	GAGAAATGGCCCTTTTACGATGTGCTCTCCACCTCTCCCTCAGGCGCGTATGGGCTCTTCA	6552
QY	5413	AACCTCTGTGGCGGAGGAGTGGCGGGAACATCACCGCGTGGAGTCAGAAATAAG				

Db 7141 GAGAAATGGCCCTTTACGATGTGCTCCACCCCTCCCTCAGCGCGTGATGGCTCTTCA 7200
QY 6553 TACCGAATCCAAATCTCTCTGACACGCGGTGAGTTCCTGTGTAATGCCTGGAAAGCG 6612
Db 7201 TACCGAATCCAAATCTCTCTGACACGCGGTGAGTTCCTGTGTAATGCCTGGAAAGCG 7260
QY 6613 AAGAAATGCCCTATGGGCTTCGATATGACACCCGCTGTTTTGACTCAACGGTCACTGAG 6672
Db 7261 AAGAAATGCCCTATGGGCTTCGATATGACACCCGCTGTTTTGACTCAACGGTCACTGAG 7320
QY 6673 AATGATATCCGCTGTTGAGGAGTCAATCTACCAATCTGTGACTTGGCCGCCGAAAGCAGA 6732
Db 7321 AATGATATCCGCTGTTGAGGAGTCAATCTACCAATCTGTGACTTGGCCGCCGAAAGCAGA 7380
QY 6733 CAGGCCATAAGGTCTGCTCACAGAGCGGCTTTACATCGGGGGCCCTGACTAAATCTAAA 6792
Db 7381 CAGGCCATAAGGTCTGCTCACAGAGCGGCTTTACATCGGGGGCCCTGACTAAATCTAAA 7440
QY 6793 GGGCAGAACTCGGCTATCGCGGTGCGCGAGCGGTGACTGACGACCAAGCTGCGGT 6852
Db 7441 GGGCAGAACTCGGCTATCGCGGTGCGCGAGCGGTGACTGACGACCAAGCTGCGGT 7500
QY 6853 AATACCCCTCACATGTTACTTGAAGCCCGCTGCGCGCTGTCGAGCTGCGAAGCTCAGAC 6912
Db 7501 AATACCCCTCACATGTTACTTGAAGCCCGCTGCGCGCTGTCGAGCTGCGAAGCTCAGAC 7560
QY 6913 TGCAGATGCTGATGCGGAGACGACCTTGTGTTATCTGTGAAAGCGCGGACCCAA 6972
Db 7561 TGCAGATGCTGATGCGGAGACGACCTTGTGTTATCTGTGAAAGCGCGGACCCAA 7620
QY 6973 GAGCAGAGCGGACCTACGGCCCTTACGGAGCGTATGACTAGTACTCTGCCGCCCT 7032
Db 7621 GAGCAGAGCGGACCTACGGCCCTTACGGAGCGTATGACTAGTACTCTGCCGCCCT 7680
QY 7033 GGGGACCGCCGCAACAGAAATACGACTTGGAGTTGATTAACATCATGCTCTCCAATGTG 7092
Db 7681 GGGGACCGCCGCAACAGAAATACGACTTGGAGTTGATTAACATCATGCTCTCCAATGTG 7740
QY 7093 TCACTGCGCAGATGATCGCAAGGCTGACTATCTCAACGCGTACCCGACCCACCC 7152
Db 7741 TCACTGCGCAGATGATCGCAAGGCTGACTATCTCAACGCGTACCCGACCCACCC 7800
QY 7153 CCCCTGCGCGGCTCGGTGGGAGACGCTAGACACATCCAGTCAATCTCGCTAGGC 7212
Db 7801 CCCCTGCGCGGCTCGGTGGGAGACGCTAGACACATCCAGTCAATCTCGCTAGGC 7860
QY 7213 AACATCATGATGATGCGCCACCTTGTGGCAAGGATGATCTGATGACTCATTTCTTC 7272
Db 7861 AACATCATGATGATGCGCCACCTTGTGGCAAGGATGATCTGATGACTCATTTCTTC 7920
QY 7273 TCACTGCTTCTAGCTCAGAAACAACTTGAAGGCTTGAATGTCAGATCTACGGGCG 7332
Db 7921 TCACTGCTTCTAGCTCAGAAACAACTTGAAGGCTTGAATGTCAGATCTACGGGCG 7980
QY 7333 TGTACTCATTGAGCCTTACCTACCTCAGATCAATTCACGACTCCATGCGCTTAGC 7392
Db 7981 TGTACTCATTGAGCCTTACCTACCTCAGATCAATTCACGACTCCATGCGCTTAGC 8040
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Db 8041 GCATTTTCACTCCATGATGATCTCCAGTGAATCAATAGGCTGCTTATGCTCAGG 8100
QY 7453 AAACCTGGGCTACCGCCCTTGGAGTCTGGAGACATCGGGCCAGAAAGTGTCCGCGCTAGG 7512
Db 8101 AAACCTGGGCTACCGCCCTTGGAGTCTGGAGACATCGGGCCAGAAAGTGTCCGCGCTAGG 8160
QY 7513 CTACTGCTCCAGGGGGAGGCTGCACTTGTGGCAAGTACCTCTTCAACTGGGCACTA 7572
Db 8161 CTACTGCTCCAGGGGGAGGCTGCACTTGTGGCAAGTACCTCTTCAACTGGGCACTA 8220
QY 7573 AGGACCAAGCTCAAACTCACTCCAAATCCCGGCTGCTCCAGTTGGATTTATCAGCTGG 7632
Db 8221 AGGACCAAGCTCAAACTCACTCCAAATCCCGGCTGCTCCAGTTGGATTTATCAGCTGG 8280

QY 7633 TTCTGTGCTGTTTACAGCGGGGAGACATATATCACAGCTGCTCTCGTCCGACCCCGC 7692
Db 8281 TTCTGTGCTGTTTACAGCGGGGAGACATATATCACAGCTGCTCTCGTCCGACCCCGC 8340
QY 7693 TGGTTTCATGTGTGCTGCTACTCTTCTGTAGGGTAGGCATCTATCTATCTCCCAAC 7752
Db 8341 TGGTTTCATGTGTGCTGCTACTCTCTTCTGTAGGGTAGGCATCTATCTATCTCCCAAC 8400
QY 7753 CGATGAAACGGGAGCTTAAACACTCCAGGCAATAGGCCATCTGTTTTTCCCTTTT 7812
Db 8401 CGATGAAACGGGAGCTTAAACACTCCAGGCAATAGGCCATCTGTTTTTCCCTTTT 8460
QY 7813 TTTTCTT 7872
Db 8461 TTTTCTT 8520
QY 7873 TTTTCTT 7932
Db 8521 TTTTCTT 8580
QY 7933 GTCCGTGAGCGCTTGACTGAGAGAGTGTGATGATGAGTGGCTCTCTGAGATCAAGT 7989
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RESULT 15
AX036253
LOCUS AX036253 8637 bp DNA linear PAT 16-NOV-2000
DEFINITION Sequence 2 from Patent EP1043399.
ACCESSION AX036253
VERSION AX036253.1 GI:11225869
KEYWORDS
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
Virus; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.

REFERENCE 1
AUTHORS Bartenschlager R.D.
TITLE Hepatitis C virus cell culture system
JOURNAL Patent: EP 1043399-A 2 11-OCT-2000;
BARTENSCHLAGER RALF DR (DE)
FEATURES
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ORIGIN

Query Match 91.6%; Score 7324.6; DB 6; Length 8637;
Best Local Similarity 92.5%; Pred. No. 0;
Matches 7985; Conservative 0; Mismatches 4; Indels 648; Gaps 1;

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Db 61 TCTTCACGAGAAAGCGTCTAGCCATGGCTTAGTATGAGTGTCTGAGCCCTCCAGGAC 120
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QY	301	GTCTTTGCGAGTCCCGGAGGTCTCGTAGACCGTGACCATGAGCAAGATCCTAAAC	360	Db	1381	AGGGGTCTTTCCCTCTCGCCAAAGGAATGCAAGGTCTGTGTAATGTCTGAAGGAGCA	1440
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QY	361	CTCAAGAAAAACAAAGGCGCGCCATGATTGAACAGATGATTCACGAGGTTCTC	420	Db	1441	GTTTCCTCTGGAAGCTTCTTGAAGCAAAACAACTCTGTAGCGACCTTTTGCAGCGCGG	1500
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QY	421	CGGCGGTTGGGTGGAGAGCTATTTCGCTATGATCGGCAACACAGACATCGGCTGCT	480	Db	1501	AACCCCCACCTGGCGACAGGTGCTCTGCGGCCAAAGCAACGCTGTATAGATACACCT	1560
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QY	541	ACCTGTCCGGTCCCTGATGAATGACATGACGAGGAGGCGCGGCTATCGTGGCTGGCCA	600	Db	1621	TGGCTCTCTCCTCAGCGGTATTCAACAGGGGCTGAAGGATGCCAGAGGTACCCCATGT	1680
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QY	601	CGAGCGGTTCCCTTGCAGCTGTGCTCGACGTTGTCACTGAAGCGGAAAGGACTGGC	660	Db	1681	ATGGGATCTGATCTGGGCGCTCGGTGCAATGCTTTTACATGTGTAGTTCGAGGTTAAA	1740
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QY	721	AAGTATCATATGCTGATGCAATGCGGCGGAGGATCTCTGTCTCATCTTCTCTGCG	780	Db	1801	ATGGACCGGAGATGGAGCATCTGCGGAGGCGGGTTTTCGTAGTCTGATACCTCTTG	1860
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QY	841	TTGTGATCAGGATGATCTGAGAGAGCATCAGGGGCTCGGCGAGCGAACTGTTTCG	900	Db	1921	ATCACCGGCGGAGCACATTGCAAGTGTGATCCCCCCTCAACGTTGGGGGGG	1980
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QY	901	CGAGGCTAAGGCGGCGATGCGCGAGGAGATCTCGTACCCATGGCGATGCTT	960	Db	1981	CGCGATGCGCTCATCTCTCTCAGTGGCGATCCACCCAGAGCTAATCTTTACCATCACC	2040
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QY	961	GCTTCCGGAATATCATGTTGGAATGCGCGCTTTTCTGGAATCATCGACTGTGGCGGC	1020	Db	2041	AAAATCTGTGCGGCATCTCGGTCCACTCATGGTCTCCAGGCTGGTATACCAAGTG	2100
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QY	1141	AGCGATCGCTTCTATCGCTTCTTGACGAGTTCTTCTGAGTTTAAACAGACCAACG	1200	Db	2221	TATGACCATCTCACCCCACTGCGGAGTGGGCGCACCGGGCCCTACGAGACCTTTCGCGTG	2280
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QY	1381	AGGGGTCTTTCCCTCTCGCCAAAGGAATGCAAGGTCTGTTGAATGTCTGAAGGAGCA	1440				

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Db	2521	CGGACAGAAACAGATCGAGGGGAGGTCCAGGTGCTTCCACCGCAACACAATCTTTC	2580
QY	1933	CTGGGACCTGGTCAATGGCGTGTGTGGACTGTCTATCATGGTCCGGCTCAAGACC	1992
Db	2581	CTGGGACCTGGTCAATGGCGTGTGTGGACTGTCTATCATGGTCCGGCTCAAGACC	2640
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Db	2641	CTTGGCGGCGCCAAAGGGCCCAATCACCCAAATGTACACCAATGTGGACAGACCTCGTC	2700
QY	2053	GGCTGGCAAGCCCGCCCGGGCGGCTTCTTTGACACCAATGACCTTGGCGAGCTCGGAC	2112
Db	2701	GGCTGGCAAGCCCGCCCGGGCGGCTTCTTTGACACCAATGACCTTGGCGAGCTCGGAC	2760
QY	2113	CTTTACTTGGTCACAGGACATGCCGATGTCAATTCGGGTGGCGGCGGACAGCAGG	2172
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QY	2173	GGGAGCCTACTCTCCCGCAGGCGGCTCTCTACTTTGAAGGGCTCTTCCGGCGGTCCACTG	2232
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QY	2233	CTCTGCCCTCTGGGCGACAGCTGTGGGCACTCTTTTGGGCTGCCGTGTGACCCGAGGGGT	2292
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QY	2293	GCGAAGCGGTGGATTGTACCGGTGAGTCTATGGAACCACTATGCGGTGCCCGGCTC	2352
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QY	2353	TTACAGGACAACTCGTCCCTCCGCGGTACCGGTGAGTCTATGGAACCACTATGCGGTGCCCGGCTC	2412
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QY	2533	AAGGCAATGGTATCGAACCTTAACATCAGAACCGGGTAAAGACCATCAACAGGGTGC	2592
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QY	3073	TCAGTGATCGACTCGCAATACATGTCTACCCAGACAGTGCATTCAGCCTGGACCGGAC	3132
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QY	3133	TTACCATTTGAGACGACGACCGTGTCCACAAAGACGGTGTACCTTCCAGGAGAACGGCCCTCG	3192
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QY	3193	AGGACTGTAGGGCAGGATGGGCAATTTACAGGTTTGTGACTTCCAGGAGAACGGCCCTCG	3252
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QY	3433	GCCCATTTCTTGTCTCCAGACTTAAGCAGCAGGAGACACTTCCCTTACCTGGTAGATAC	3492
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QY	3493	CAGCTACGTTGTGCGCCAGGCTCAGGCTCCACTCCATCTGTTGGGACCAAAATGTGAG	3552
Db	4141	CAGCTACGTTGTGCGCCAGGCTCAGGCTCCACTCCATCTGTTGGGACCAAAATGTGAG	4200
QY	3553	TGTCTCATACGGCTAAGCCCTAGCTGCAAGGCGCAACGCGCTTGTGTATAGCTGGGA	3612
Db	4201	TGTCTCATACGGCTAAGCCCTAGCTGCAAGGCGCAACGCGCTTGTGTATAGCTGGGA	4260
QY	3613	GCGTTTCAAAAACAGGTTTACTACACACACCCCATCAACCAATACATCATGCGATG	3672
Db	4261	GCGTTTCAAAAACAGGTTTACTACACACACCCCATCAACCAATACATCATGCGATG	4320
QY	3673	TCGGCTGACCTGGAGTGTCTGACGACCTGCGGTGCTGTGTAGGCGGAGTCTTAGCAGT	3732
Db	4321	TCGGCTGACCTGGAGTGTCTGACGACCTGCGGTGCTGTGTAGGCGGAGTCTTAGCAGT	4380
QY	3733	CTGGCGCGTATTTGCTGACAAACAGCAGCGGTGCTTGTGGGAGGATCATCTTTGTC	3792
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QY	3793	GGAGCGCGGCTCATTTTCCGACAGGGAAGTCTTTTACCGGAGTTCGATGAGATGAA	3852
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QY	3853	GAGTGGGCTCACCTCTTTCATCGAAACAGGGAATGACGTGCGCGCAAAATTCAA	3912
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QY	3973	GTGGAATCAAAGTGGCGACCTCGAGGCTTCTGGGCGAGACATATGTGGAATTCATC	4032
Db	4621	GTGGAATCAAAGTGGCGACCTCGAGGCTTCTGGGCGAGACATATGTGGAATTCATC	4680

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QY	4153	AACATCTTGGGGGATGGGTGGCGCCCAACTTCTCTCCACGCGTGTCTTGTCTTTC	4212	Db	5881	GTGCTCACTTCCATGTCTACCGACCCCTCCCAATTAACGGCGGAGACGGCTAAGCGTAGG	5940
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QY	4213	GTAGCGCGCGCATGCGTGGAGCGGCTGTGGAGCATAGACCTTGGAGAGTCTTGTG	4272	Db	5941	CTGCGCAAGGGATCTCCCTCTCTTGGCCAGCTCATCAGCTAGCCAGCTGTCTGCGCT	6000
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QY	4333	AGCGCGAGATGCCCTCCACCGAGACCTGGCTAACTACTCCCTGTCTATCTCTCCCT	4392	Db	6061	AACCTCTCTGTGGCGGAGGATGGCGGGAAACATCACCCGCTGGAGTTCAGAAATAAG	6120
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QY	4393	GGCGCCCTAGTCTCGGGTCTGTGGCAGGATCTCGCTCGCGACGCTGGGGCCAGGG	4452	Db	6121	GTAGTAATTTTGGACTCTTTTCGAGCGCTCCAAAGCGGAGGAGTGAAGAGGAATATCC	6180
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QY	4453	GAGGGGCTGTGACGTGGATGAACCGCTGATAGGCTTCGCTTCGCGGGGTAAACACGTC	4512	Db	6181	GTTCGCGCGGAGATCCTCGGAGGTCCAGGAAATTCCTCGAGCGATGCCATATGGGA	6240
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QY	4513	TCCTCCACACACTATGTCTCGAGCGACGCTGACGACGCTGCTGCTGCTGCTGCTGCT	4572	Db	6241	CGCCCGGATTAACACCCCTCACTGTAGAGTCTCGAGGAGCCCGACTTACCTCCCTCCA	6300
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QY	4573	AGTCTTACACTCAGCTGCTGAAGAGCTTCAACAGTGGATCAACGAGGACTGCTCC	4632	Db	6301	GTGGTACAGCGGTGTCATTGCGCTGCAAGGCGCTCCGATACCACTCCACGGAGG	6360
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QY	4633	AGCCATGCTCCGGCTCTGGCTTAAGAGATGTTTGGGATTGGAATGACGCTGTTGACT	4692	Db	6361	AAGAGGACGGTGTCTCTGTCAAGATCTACCGTGTCTTCTGCTTGGCGGAGTCCGCCACA	6420
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QY	4693	GAITTCAGACCTGGCTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGT	4752	Db	6421	AAGACCTTCCGAGCTCCGAAATCGTGGCGCTCGACGCGGACGCGCAACGGGCTCTCT	6480
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QY	4753	TCATGTCACAGTGGGTACAGGAGTCTGGCGGGGACGCGCATCATGCAAAACACCTGC	4812	Db	6481	GACCGCCCTCCGACGACGCGGATCCGATCTCAGCGACCGGCTTGGTCTACCGTAAGC	6540
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QY	4813	CCATGTTGAGCAGATCACCGGACATGTGAAAGGTTCCATGAGGATCGTGGGGCT	4872	Db	6541	CCCTTTGAGGGGAGCGGGGATCCCGATCTCAGCGACCGGCTTGGTCTACCGTAAGC	6600
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QY	4933	TGCACGCCCTCCCGCGCCCAATTTATTTAGGCGCTGTGGCGGGTGGCTGTGAGGAG	4992	Db	6661	ATCACGCCATGCGCTGGAGGAAACCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	6720
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Db	5641	TACGTGAGGTTAGCGGGTGGGGATTTTCCACTACGTGAGCGGGATGACCACTGACAC	5700	QY	6133	AAGGTCACTTTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	6192
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QY 6373 GAGACACCAATTTGACACACACATCATGGAAGAGAGTTTCTGCGTCCAAACAGAG 6432
Db 7021 GAGACACCAATTTGACACACACATCATGGAAGAGAGTTTCTGCGTCCAAACAGAG 7080
QY 6433 AAGGGGGCGCGCAAGCCAGCTCGCTTATCGTATTTCCAGATTTGGGGGTTCTGTTGTC 6492
Db 7081 AAGGGGGCGCGCAAGCCAGCTCGCTTATCGTATTTCCAGATTTGGGGGTTCTGTTGTC 7140
QY 6493 GAGAAATGGCCCTTTACGATGGTCTCCACCTCCCTCAGCCGCTGATGGGCTCTTCA 6552
Db 7141 GAGAAATGGCCCTTTACGATGGTCTCCACCTCCCTCAGCCGCTGATGGGCTCTTCA 7200
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Search completed: August 12, 2004, 09:38:29
Job time : 19781 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 12, 2004, 02:12:50 ; Search time 1827 Seconds
(without alignments)
18583.251 Million cell updates/sec

Title: US-10-005-469-4

Perfect score: 7992

Sequence: 1 gccagccccgattgggggc.....ctctctgcagatcaagtact 7992

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2003as:*
- 8: Geneseqn2003bs:*
- 9: Geneseqn2003cs:*
- 10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	7985.6	99.9	7992	6	AAL47276 Hepatitis
2	7985.6	99.9	10690	6	Abk91412 Hepatitis
3	7985.6	99.9	10690	8	ACA61697 Hepatitis
4	7985.6	99.9	10690	9	ADC83762 pHCVNeol7
5	7984	99.9	7992	6	AAL47281 Hepatitis
6	7984	99.9	10690	6	Abk91448 Hepatitis
7	7984	99.9	10690	6	Abk91435 Hepatitis
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10	7982.6	99.9	7989	3	Abk91434 Hepatitis
11	7982.4	99.9	10690	6	Abk91440 Hepatitis
12	7981	99.9	7989	6	AAL47277 Hepatitis
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16	7979.4	99.8	7989	6	AAL47279 Hepatitis
17	7977.6	99.8	10690	6	AAL47279 Hepatitis
18	7976.2	99.8	7989	6	AAL47279 Hepatitis
19	7976.2	99.8	7989	6	AAL47279 Hepatitis
20	7974.6	99.8	10691	6	Abk91423 Hepatitis
21	7972.6	99.8	10693	6	Abk91438 Hepatitis
22	7971	99.7	10693	6	Abk91443 Hepatitis
23	7969.8	99.7	10691	6	Abk91439 Hepatitis

24	7968.6	99.7	7987	6	AAD25321 Hepatitis
25	7967	99.7	7987	6	AAD25329 Hepatitis
26	7965.4	99.7	7987	6	AAD25324 Hepatitis
27	7961.4	99.6	7995	6	AAL47278 Hepatitis
28	7960.6	99.6	8001	3	AAA98967 Hepatitis
29	7771.4	97.2	7989	9	ADD93733 Hepatitis
30	7689	96.2	7848	6	AAD25323 Hepatitis
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38	7302.6	91.4	8649	3	AAA98969 Hepatitis
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41	7246.6	90.7	8638	6	ABK8578 Hepatitis
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43	7242	90.6	8642	6	ABK8574 Hepatitis
44	7239.2	90.6	8638	6	ABK8577 Hepatitis
45	7223.4	90.4	8648	6	ABK8576 Hepatitis

ALIGNMENTS

RESULT 1

AAL47276

ID AAL47276 standard; DNA; 7992 BP.

XX AAL47276;

AC AAL47276;

XX 30-AUG-2002 (first entry)

XX Hepatitis C virus sub-genomic replicon clone I377-NS3-3'UTR.

DE Hepatitis C virus sub-genomic replicon clone I377-NS3-3'UTR.

XX Hepatitis; HCV; core-neo; NS3 proteinase/helicase; vaccine; diagnosis;

KW virucide; hepatotropic; gene therapy; anti-viral; gene; ds.

XX Hepatitis C virus.

OS Hepatitis C virus.

XX Key Location/Qualifiers

PH CDS 342..1181

FT /*tag= a

FT /product= "core-neo fusion protein"

FT 1801..7758

FT /*tag= b

FT /product= "NS3 proteinase/helicase"

XX WO200238793-A2.

XX 16-MAY-2002.

PD Adc83762 pHCVNeol7

XX 02-NOV-2001; 2001WO-US046350.

PF Abk91448 Hepatitis

XX 07-NOV-2000; 2000US-0245866P.

PR (ANAD-) ANADYS PHARM INC.

XX Bichko V;

XX WPI; 2002-490082/52.

XX P-PSDB; AAC18000, AAC18001.

XX Novel nucleic acid encoding replication competent recombinant hepatitis C

XX virus genome useful for screening anti-hepatitis C virus therapeutics and

XX for vaccine development.

XX Claim 6; Page 43-47; 85pp; English.

XX The present invention provides protein and coding sequences from

XX Hepatitis C virus (HCV), comprising all or part of the HCV genome and

CC

CC able to replicate efficiently when transfected into a susceptible cell
 CC line without reducing the growth rate of the cell line by more than 10
 CC fold. The sequences are useful for screening for anti-HCV therapeutics,
 CC for detecting antibodies to HCV in a biological sample such as blood,
 CC serum, plasma, blood cells, lymphocytes, or liver cells from a subject,
 CC for deriving authentic HCV components such as replication-complement non-
 CC infectious, replication-defective infection-component, and replication-
 CC defective non-infectious HCV, in gene therapy or gene vaccination
 CC targeted to hepatic tissue for treating an animal infected or susceptible
 CC to HCV infection and for studying HCV infection and propagation. The
 CC present sequence is a clone of a fragment of the HCV genome which encodes
 CC the core-neo and NS3 proteinase/helicase proteins
 XX

SQ Sequence 7992 BP; 1648 A; 2369 C; 2243 G; 1732 T; 0 U; 0 Other;
 Query Match 99.9%; Score 7985.6; DB 6; Length 7992;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 7988; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 GCCAGCCCCGATTGGGGGCGACACTCCACCATAGATCACTCCCTGTGAGGAATCTG 60
 DB 1 GCCAGCCCCGATTGGGGGCGACACTCCACCATAGATCACTCCCTGTGAGGAATCTG 60
 QY 61 TCTTACGCGAAGAGCGTCTAGCCATGCGGTAGTATGAGTGTGCTGAGCTCCAGGAC 120
 DB 61 TCTTACGCGAAGAGCGTCTAGCCATGCGGTAGTATGAGTGTGCTGAGCTCCAGGAC 120
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 DB 121 CCCCCCTCCGGGAGAGCCATAGTGTCTGCGGAACCGGTAGTACACCGGAATTCGCAG 180
 QY 181 GACGACCGGCTCTTCTTGGATCAACCGCTCAATGCTGAGATTTGGGGGTGCCCC 240
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 QY 241 GCGAGCTGTAGCGAGTAGTGTGGTTCGCGAAGGCTTGTGCTACTGCTGATAGG 300
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 QY 1141 AGCGCATCGCTTCTATCGCGCTTCTGACGAGTCTTCTGAGTTTAAACAGACCAACG 1200
 DB 1141 AGCGCATCGCTTCTATCGCGCTTCTGACGAGTCTTCTGAGTTTAAACAGACCAACG 1200
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Db 7981 AGATCAAGTACT 7992
RESULT 2
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XX
AC ABK91412;
XX
DT 15-NOV-2002 (first entry)
XX
DE Hepatitis C virus vector construct pHVNeo.17.
XX
KW HCV; ss; pHVNeo.17; adaptive mutation; liver failure; cirrhosis;
KW hepatocellular carcinoma; NS3; NS5; encephalomyocarditis virus; EMCV;
KW internal ribosome entry site; IRES; NS5A; HCV replication.
XX
OS Hepatitis C virus.
OS Encephalomyocarditis virus.
OS Escherichia coli.
OS Enterobacteria phage T7.
XX
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/*tag= c
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Mon Aug 16 09:32:31 2004

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FT CDS
FT /tag= d
FT /product= "Polyprotein"
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FT 3'UTR
FT /tag= e
FT /tag= f
FT /note= "Plasmid derived sequences"
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XX
XX 16-JAN-2002; 2002WO-EP000526.
XX
XX 23-JAN-2001; 2001US-0263479P.
XX
XX (RICE-) IST RICERHE BIOL MOLECOLARE ANGELETTI.
XX
XX De Francesco R, Migliaccio G, Paonessa G;
XX
XX WPI; 2002-599793/64.
XX
XX New Hepatitis C virus (HCV) replicons comprising altered HCV NS3 or HCV
XX NS5 encoding region, or encephalomyocarditis virus (EMCV) internal
XX ribosome entry site (IRES) region, useful in studying HCV replication and
XX expression.
XX
XX Claim 1; Fig 1; 69pp; English.
XX
XX The invention relates to nucleic acid molecules comprising altered HCV
XX NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV)
XX internal ribosome entry site (IRES) region coding for one or more NS3,
XX NS5A, or EMCV IRES mutations, respectively. The location of the mutations
XX are detailed in the specification. Also included are (1) an expression
XX vector comprising a nucleotide sequence coding for the altered nucleic
XX acids, which is transcriptionally coupled to an exogenous promoter; (2) a
XX recombinant cell human hepatoma cell comprising the altered nucleic acids
XX; (3) a recombinant cell produced by introducing into a human hepatoma
XX cell the altered nucleic acids; (4) producing an HCV (hepatitis C virus)
XX replicon enhanced cell or which containing a functional HCV replicon; (5)
XX an HCV replicon enhanced cells made in the method; and (6) measuring the
XX ability of a compound to affect HCV activity. The HCV replicons and HCV
XX replicon enhanced cells are useful in studying HCV replication and
XX expression, and providing a system for measuring the ability of a compound
XX to modulate one or more HCV activities e.g. to discover drugs which may
XX treat HCV mediated diseases such as liver failure, cirrhosis and
XX hepatocellular carcinoma. The present sequence is the HCV based vector
XX pHCVNeo.17, used as a basis for the adaptive mutations of the invention
XX
XX SQ Sequence 10690 BP; 2334 A; 3045 C; 2908 G; 2403 T; 0 U; 0 Other;
XX
XX Query Match 99.9%; Score 7985.6; DB 6; Length 10690;
XX Best Local Similarity 99.9%; Pred. No. 0;
XX Matches 7988; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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XX QY 1 GCCAGCCCGGATGGGGGACACCTCCACATAGATCACTCCCTGTGAGGAACACTG 60
XX DB 1 GCCAGCCCGGATGGGGGACACCTCCACATAGATCACTCCCTGTGAGGAACACTG 60
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XX DB 61 TCTTACGAGAGAAGCGTCTAGCCATGGCGTTATAGTATAGTGTGCGAGCCTCCAGGAC 120
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Db	3061	GG	CGATTT	CGA	CTC	AGT	GTAT	CG	ACT	GCA	3120
QY	3121	CT	GACCG	CA	CTTCA	CCAT	TG	AG	ACG	CG	3180
Db	3121	CT	GACCG	CA	CTTCA	CCAT	TG	AG	ACG	CG	3180
QY	3181	CAG	CGCGAG	CAG	CACTG	TAG	GGC	AGG	ATG	GGC	3240
Db	3181	CAG	CGCGAG	CAG	CACTG	TAG	GGC	AGG	ATG	GGC	3240
QY	3241	GA	ACGGCC	CTCG	GGCAT	GTTC	GA	TTCC	TCT	GTG	3300
Db	3241	GA	ACGGCC	CTCG	GGCAT	GTTC	GA	TTCC	TCT	GTG	3300
QY	3301	GC	TTGGTAC	GAG	CTCA	CGCC	CG	CGAG	CA	CTC	3360
Db	3301	GC	TTGGTAC	GAG	CTCA	CGCC	CG	CGAG	CA	CTC	3360
QY	3361	CC	AGGTTGCC	CTCT	GC	AGG	AC	CA	TCT	GG	3420
Db	3361	CC	AGGTTGCC	CTCT	GC	AGG	AC	CA	TCT	GG	3420
QY	3421	AC	CCACATAG	ACGCC	CA	TTCT	GT	CC	CAG	ACT	3480
Db	3421	AC	CCACATAG	ACGCC	CA	TTCT	GT	CC	CAG	ACT	3480

QY	3481	CTGGTAGCATACAGGCTACGGTGTGGCGCAGGGCTCAGGCTCCACTCCATCGTGGAC	3540	4561	CACATCCTCTAGTCTTACCATCACTCAGCTCTGAAGAGGCTTCCACAGTGATCAAC	4620	
Db	3481	CTGGTAGCATACAGGCTACGGTGTGGCGCAGGGCTCAGGCTCCACTCCATCGTGGAC	3540	QY	4621	GAGGACTGCTCCAGCGCATGCTCCGGCTCGTGAAGAGATGTTGGGATGGATATGC	4680
QY	3541	CAAAATGTGGAAGTGTCTCATACGGCTTAAGCCTACGCTGACCGGCCAACCGCCCTGCTG	3600	Db	4621	GAGGACTGCTCCAGCGCATGCTCCGGCTCGTGAAGAGATGTTGGGATGGATATGC	4680
Db	3541	CAAAATGTGGAAGTGTCTCATACGGCTTAAGCCTACGCTGACCGGCCAACCGCCCTGCTG	3600	QY	4681	ACCGTGTGACTGANTTTCAAGACCTGGCTCCAGTCCAAAGCTCTGCGCGGATTCGCGGGA	4740
QY	3601	TATAGGCTGGAGCCGTTCAAAACGAGGTTACTACACACACACCCCAATAACATC	3660	Db	4681	ACCGTGTGACTGANTTTCAAGACCTGGCTCCAGTCCAAAGCTCTGCGCGGATTCGCGGGA	4740
Db	3601	TATAGGCTGGAGCCGTTCAAAACGAGGTTACTACACACACACCCCAATAACATC	3660	QY	4741	GTCCCTTCTTCTCATGTCAACGGGTACAAAGGAGTCTGGCGGGCGACGATCATG	4800
QY	3661	ATGGCATGCATGTCCGCTGACCTGGAGGTGTCAAGAGACCTGGGTCTGGTAGGCGGA	3720	Db	4741	GTCCCTTCTTCTCATGTCAACGGGTACAAAGGAGTCTGGCGGGCGACGATCATG	4800
Db	3661	ATGGCATGCATGTCCGCTGACCTGGAGGTGTCAAGAGACCTGGGTCTGGTAGGCGGA	3720	QY	4801	CAAAACACCTGCCCCTGAGGACAGATCACCGGACATGTGAAGAAAGGTTCCATGAGG	4860
QY	3721	GTCTAGAGCTCTGGCGCGGTATGCTGACACAGCAGCGGTGCTTATGTTGGGAGG	3780	Db	4801	CAAAACACCTGCCCCTGAGGACAGATCACCGGACATGTGAAGAAAGGTTCCATGAGG	4860
Db	3721	GTCTAGAGCTCTGGCGCGGTATGCTGACACAGCAGCGGTGCTTATGTTGGGAGG	3780	QY	4861	ATCGTGGGGCTTAGGACCTGTAGTAAACAGTGGATGGAACATTTCCCATTAACGCTAC	4920
QY	3781	ATCATCTTGTCCGGAAGCCCGCCATCATCTCCGACAGGGAAGTCTTTACCGGAGTTC	3840	Db	4861	ATCGTGGGGCTTAGGACCTGTAGTAAACAGTGGATGGAACATTTCCCATTAACGCTAC	4920
Db	3781	ATCATCTTGTCCGGAAGCCCGCCATCATCTCCGACAGGGAAGTCTTTACCGGAGTTC	3840	QY	4921	ACCAAGCGCCCTGCAAGCCCTCCCGCGCCAAATTTATTTAGGGCCCTGTGGCGGTG	4980
QY	3841	GATGAGTGGAGAGTGCCTCTACACCTCCCTTATCATCGAACAGGGAATGAGCTCGCC	3900	Db	4921	ACCAAGCGCCCTGCAAGCCCTCCCGCGCCAAATTTATTTAGGGCCCTGTGGCGGTG	4980
Db	3841	GATGAGTGGAGAGTGCCTCTACACCTCCCTTATCATCGAACAGGGAATGAGCTCGCC	3900	QY	4981	GCTGCTGAGGAGTACGTGGAGGTTACGCGGGTGGGGGATTTCCACTAGTGAACGCGCATG	5040
QY	3901	GAACAATTCACACAGAGGCAATCGGTTGCTGCAACAGCCACCAAGCAGCGAGGCT	3960	Db	4981	GCTGCTGAGGAGTACGTGGAGGTTACGCGGGTGGGGGATTTCCACTAGTGAACGCGCATG	5040
Db	3901	GAACAATTCACACAGAGGCAATCGGTTGCTGCAACAGCCACCAAGCAGCGAGGCT	3960	QY	5041	ACCACTGACAACTAAAGTGGCGGCTGTGAGTTCGGGCGCCCGAAATTTCTTCAAGAGTG	5100
QY	3961	GCTGCTCCGCTGCTGAAATCCAAATGCGGGAACCTCGAAGCCTTCTGGCGGAAGATATG	4020	Db	5041	ACCACTGACAACTAAAGTGGCGGCTGTGAGTTCGGGCGCCCGAAATTTCTTCAAGAGTG	5100
Db	3961	GCTGCTCCGCTGCTGAAATCCAAATGCGGGAACCTCGAAGCCTTCTGGCGGAAGATATG	4020	QY	5101	GATGGGTGCGGTGACAGGTACCGTCCAGCGTGCMAACCCCTCTACGCGAGGAGTTC	5160
QY	4021	TGGAATTTTCATCAGCGGGATCAATATTTAGCAGGTTGTCACTCTGCTGGCAACCC	4080	Db	5101	GATGGGTGCGGTGACAGGTACCGTCCAGCGTGCMAACCCCTCTACGCGAGGAGTTC	5160
Db	4021	TGGAATTTTCATCAGCGGGATCAATATTTAGCAGGTTGTCACTCTGCTGGCAACCC	4080	QY	5161	ACATTCCTGCTCGGCTCAATCAATACCTGTTGGTTCACAGCTCCCATCGAGCCGAA	5220
QY	4081	GGATAGATCACTGATGCAATTCACAGCTCTATCACCAGCCCGCTCACCAACCCAAAT	4140	Db	5161	ACATTCCTGCTCGGCTCAATCAATACCTGTTGGTTCACAGCTCCCATCGAGCCGAA	5220
Db	4081	GGATAGATCACTGATGCAATTCACAGCTCTATCACCAGCCCGCTCACCAACCCAAAT	4140	QY	5221	CCGAGCTAGAGTGTCTCACTTCCATGCTACCGACCCCTCCCAATTAAGCGGAGAGG	5280
QY	4141	ACCTCTCTGTTAAATCTGCGGGGATGGGTGGCGCCCAACTTCTCTCCAGCGCT	4200	Db	5221	CCGAGCTAGAGTGTCTCACTTCCATGCTACCGACCCCTCCCAATTAAGCGGAGAGG	5280
Db	4141	ACCTCTCTGTTAAATCTGCGGGGATGGGTGGCGCCCAACTTCTCTCCAGCGCT	4200	QY	5281	GCTAAGCGTAGGCTGCGGAGGATCTCCCGCTCTTGGCCAGCTCATCAGTACGCGAG	5340
QY	4201	GCTTCTGCTTCTAGCGCGCGCATCGCTGGAGCGGCTTGGCAGCATAGGCTTGGG	4260	Db	5281	GCTAAGCGTAGGCTGCGGAGGATCTCCCGCTCTTGGCCAGCTCATCAGTACGCGAG	5340
Db	4201	GCTTCTGCTTCTAGCGCGCGCATCGCTGGAGCGGCTTGGCAGCATAGGCTTGGG	4260	QY	5341	CTGTCTGCGCTTCTTGAAGGCAACATGCACTACCGTCACTGACTCCCGGAGCGTAC	5400
QY	4261	AAGTCTGTTGATATTTTGGCAGGTTATGAGCAGGGGTGGCAGCGGCTTGGG	4320	Db	5341	CTGTCTGCGCTTCTTGAAGGCAACATGCACTACCGTCACTGACTCCCGGAGCGTAC	5400
Db	4261	AAGTCTGTTGATATTTTGGCAGGTTATGAGCAGGGGTGGCAGCGGCTTGGG	4320	QY	5401	CTCATCGAGCCAACTCTCTGTTGGCGAGGATGCGGCGGAAACATCAACCCCGTGGAG	5460
QY	4321	TTTAAAGTCAATGAGCGCGAGATGCCCTCCACCGAGGACCTGGGTAACTCTCCCTGCT	4380	Db	5401	CTCATCGAGCCAACTCTCTGTTGGCGAGGATGCGGCGGAAACATCAACCCCGTGGAG	5460
Db	4321	TTTAAAGTCAATGAGCGCGAGATGCCCTCCACCGAGGACCTGGGTAACTCTCCCTGCT	4380	QY	5461	TCAGAAATTAAGTGTAGTAAATTTTGGACTCTTTCGAGCCGCTCCAAAGCGAGGAGTACG	5520
QY	4381	ATCCTCTCCCTGCGCGCTAGTGTGCTGGGGTGTGGCGCAGGATGCTGCGGCAC	4440	Db	5461	TCAGAAATTAAGTGTAGTAAATTTTGGACTCTTTCGAGCCGCTCCAAAGCGAGGAGTACG	5520
Db	4381	ATCCTCTCCCTGCGCGCTAGTGTGCTGGGGTGTGGCGCAGGATGCTGCGGCAC	4440	QY	5521	AGGAAAGTATCCCGTTCGCGCGAGATCTTCGCGAGGTCCAGGAAATTTCCCTCGAGCGATG	5580
QY	4441	GTGGGCCAGGGAGGGGGCTGTGACGTGATGAACCGGCTGTAGCGTTGCTTCGCG	4500	Db	5521	AGGAAAGTATCCCGTTCGCGCGAGATCTTCGCGAGGTCCAGGAAATTTCCCTCGAGCGATG	5580
Db	4441	GTGGGCCAGGGAGGGGGCTGTGACGTGATGAACCGGCTGTAGCGTTGCTTCGCG	4500	QY	5581	CCCATATGGGACCGCCCGATTAACACCTTCCACTGTTAGAGTCTCTGGAAGACCCGAC	5640
QY	4501	GGTAACCAAGCTCTCCCCACGCACTATGTGCTGAGAGCGAGCGTGCAGCAGTGTCACT	4560	Db	5581	CCCATATGGGACCGCCCGATTAACACCTTCCACTGTTAGAGTCTCTGGAAGACCCGAC	5640
Db	4501	GGTAACCAAGCTCTCCCCACGCACTATGTGCTGAGAGCGAGCGTGCAGCAGTGTCACT	4560	QY	5641	TACGTCCTCTCAGTGTACGCGGTGTCCATTTGCGGCTGTCACAGGCGCTTCCGATACCA	5700
QY	4561	CAGATCCTCTCTAGTCTTACCATCACTCAGCTGCTGAAGAGGCTTACCAAGTGGATCAAC	4620				

QY	7861	TTTTCTCCTCTTTTTCCTTTTCCTTTCCCTTTGGTGCTCATCTTAGCCCTAGTCAACGC	7920
Db	7861	TTTTCTCCTCTTTTTCCTTTTCCTTTTCCTTTGGTGCTCATCTTAGCCCTAGTCAACGC	7920
QY	7921	TAGCTGTGAAGGTCCTGTAGCGCCCTTTGACTGCAGAGAGTGCTGATACCTGCCCTCTCTGC	7980
Db	7921	TAGCTGTGAAGGTCCTGTAGCGCCCTTTGACTGCAGAGAGTGCTGATACCTGCCCTCTCTGC	7980
QY	7981	AGATCAAGTACT 7992	
Db	7981	AGATCAAGTACT 7992	
 RESULT 3			
ACA61697	ID	ACA61697 standard; DNA; 10690 BP.	
XX	ACA61697;		
XX	11-AUG-2003	(first entry)	
XX	Hepatitis C virus expression plasmid pHCVNeol7.wt DNA.		
DE	Hepatitis C virus; ds; gene; thiosemicarbazone; liver inflammation;		
XX	Hepatitis C virus; ds; gene; thiosemicarbazone; liver inflammation;		
KW	liver failure; cirrhosis.		
KW	Hepatitis C virus.		
OS	Synthetic.		
XX			
Key	Location/Qualifiers		
FH	1..341		
FT	5'UTR	/tag= a	
FT		/note= "HCV 5'UTR"	
FT	misc_feature	342..1181	
FT		/tag= b	
FT		/note= "Core-neo fusion protein selectable marker"	
FT	misc_feature	1190..1800	
FT		/tag= c	
FT		/note= "Internal ribosome entry site of encephalomyocarditis virus"	
FT	CDS	1801..7758	
FT		/tag= d	
FT		/note= "HCV polypeptide coding sequence"	
FT	mat_peptide	1801..3696	
FT		/tag= e	
FT		/note= "Non-structural protein 3"	
FT	mat_peptide	3697..3858	
FT		/tag= f	
FT		/note= "Non-structural protein 4A"	
FT	mat_peptide	3859..4641	
FT		/tag= g	
FT		/note= "Non-structural protein 4B"	
FT	mat_peptide	4642..5982	
FT		/tag= h	
FT		/note= "Non-structural protein 5A"	
FT	mat_peptide	5983..7755	
FT		/tag= i	
FT		/note= "Non-structural protein 5B and RNA-dependent RNA polymerase"	
FT	3'UTR	7759..7989	
FT		/tag= j	
FT		/note= "HCV 3'UTR"	
XX			
US2003045568-A1.	PEN		
XX	06-MAR-2003.		
XX	19-APR-2002; 2002US-00125940.		
XX	20-APR-2001; 2001US-0285104P.		
XX	(ALTA/) ALTAMURA S.		
PA	(KOCH/) KOCH U.		

XX		Altamura S, Koch U;
PI		WPI; 2003-447715/42.
XX		Treating infections by hepatitis C virus and its related conditions
XX		comprises administering thiosemicarbazone compounds.
PT		
XX		Example 2; Page 9-14; 25pp; English.
PS		
XX		The invention relates to a method of treating or preventing infection by
CC		hepatitis C virus or its related conditions by delaying the onset and
CC		inhibiting replication of hepatitis C virus which comprises administering
CC		thiosemicarbazone compounds. The method is useful for treating or
CC		preventing infection by hepatitis C virus or its related conditions e.g.
CC		liver inflammation, liver failure or cirrhosis, delaying the onset and
CC		inhibiting replication of hepatitis C. The present sequence represents
CC		the hepatitis C virus expression plasmid pHCVneo17.wt DNA
XX		
XX		Sequence 10690 BP; 2334 A; 3045 C; 2908 G; 2403 T; 0 U; 0 Other;
SQ		
		Query Match 99.9%; Score 7985.6; DB 8; Length 10690;
		Best Local Similarity 99.9%; Pred.No. 0;
		Matches 7988; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY	1	GCGAGCCCCGATTGGGGGGCAGACTCCACATAGTCACTCCCTCTGAGGAATACTG 60
DB	1	GCGAGCCCCGATTGGGGGGCAGACTCCACATAGTCACTCCCTCTGAGGAATACTG 60
OY	61	TCCTTCAGCGAAGAACGGTCTAGCCATGGCGGTAGTAGTGTCGTGCAGCCTCCAGGAC 120
DB	61	TCCTTCAGCGAAGAACGGTCTAGCCATGGCGGTAGTAGTGTCGTGCAGCCTCCAGGAC 120
OY	121	CCCCCTCCC GGAGAGACCATAGTGTGTTCGGGAACCGGTGAGTACACCAGAATTGCCAG 180
DB	121	CCCCCTCCC GGAGAGACCATAGTGTGTTCGGGAACCGGTGAGTACACCAGAATTGCCAG 180
OY	181	GACGACCGGGTCCCTTTCTTGATCAAAACCCCGCTCAATGCTCGAGATTGGCGCGTGC 240
DB	181	GACGACCGGGTCCCTTTCTTGATCAAAACCCCGCTCAATGCTCGAGATTGGCGCGTGC 240
OY	241	GCGAGACTGCTAGCCGAGTAGTGTGGTTCGGAAGACCCCTTTGTGTACTGCTGTATAGG 300
DB	241	GCGAGACTGCTAGCCGAGTAGTGTGGTTCGGAAGACCCCTTTGTGTACTGCTGTATAGG 300
OY	301	GTGCTTGGAGTGTGCCCCGGGAGGTCTGTAGACCGTGCAACCATGAGCAGTAATCTTAAC 360
DB	301	GTGCTTGGAGTGTGCCCCGGGAGGTCTGTAGACCGTGCAACCATGAGCAGTAATCTTAAC 360
OY	361	CTCAAAGAAAACCAAAGGGCGGCCATGATTGAACAAGATGGAATGACACGAGTTCTC 420
DB	361	CTCAAAGAAAACCAAAGGGCGGCCATGATTGAACAAGATGGAATGACACGAGTTCTC 420
OY	421	CGGCGCGTTGGGTGGAGAGGCTATTCCGCTATGACTGGGCA CAACAGATCGGCTGCT 480
DB	421	CGGCGCGTTGGGTGGAGAGGCTATTCCGCTATGACTGGGCA CAACAGATCGGCTGCT 480
OY	481	CTGATGCCCGCGTGTTCGGCTGTACGCGCAGGGCGCCCGGTCTCTTTTGTCAAGACCG 540
DB	481	CTGATGCCCGCGTGTTCGGCTGTACGCGCAGGGCGCCCGGTCTCTTTTGTCAAGACCG 540
OY	541	ACCTGTCCGGTGCCTGAAATGAATGACGAGCAGCGCGGCTATCGTGGCTGGCCA 600
DB	541	ACCTGTCCGGTGCCTGAAATGAATGACGAGCAGCGCGGCTATCGTGGCTGGCCA 600
OY	601	CGACGGCGGCTTCCTTSCGAGCTGTGCTCGAGCTTGTCTCACTGAACGGGAAGGACTGCG 660
DB	601	CGACGGCGGCTTCCTTSCGAGCTGTGCTCGAGCTTGTCTCACTGAACGGGAAGGACTGCG 660
OY	661	TGCTATTGGCGAAGTGC CGGGCAGGATCTCTGTGTCATCTCACCTTGTCTCTGCCGAGA 720
DB	661	TGCTATTGGCGAAGTGC CGGGCAGGATCTCTGTGTCATCTCACCTTGTCTCTGCCGAGA 720

QY 721 AAGTATCCATCATGCTGATGCAATGCGCGCTGCATACGCTTGATCCGGCTACTCGC 780
Db 721 AAGTATCCATCATGCTGATGCAATGCGCGCTGCATACGCTTGATCCGGCTACTCGC 780
QY 781 CATTCGACACCAAGCGGAAATCCATCGAGGAGCAGTACTCGATGGAAGCCGGTC 840
Db 781 CATTCGACACCAAGCGGAAATCCATCGAGGAGCAGTACTCGATGGAAGCCGGTC 840
QY 841 TTGTGATCAGGATGATCTGGAAGAGAGATCAGGGGCTCGCGCGTCCGACCGGATGTCG 900
Db 841 TTGTGATCAGGATGATCTGGAAGAGAGATCAGGGGCTCGCGCGTCCGACCGGATGTCG 900
QY 901 CCAGGCTCAAGCGCGGATGCCCGAGCGGAGATCTCTGATGACCCATGCGGATGCT 960
Db 901 CCAGGCTCAAGCGCGGATGCCCGAGCGGAGATCTCTGATGACCCATGCGGATGCT 960
QY 961 GCTTCCGGAATATCATGCTGGAATGCGCGCTTTCTTGGATTCATCGACTGTGCGCGC 1020
Db 961 GCTTCCGGAATATCATGCTGGAATGCGCGCTTTCTTGGATTCATCGACTGTGCGCGC 1020
QY 1021 TGGTGTGGCGGACCGCTATCAGGACATAGCGTGTGGCTACCGCTGATATTCGTAAGAGC 1080
Db 1021 TGGTGTGGCGGACCGCTATCAGGACATAGCGTGTGGCTACCGCTGATATTCGTAAGAGC 1080
QY 1081 TTGCGCGGATGCGCTGACCGCTTCTGCTGCTTTACGGTATCGCGCTCCCGATTGCG 1140
Db 1081 TTGCGCGGATGCGCTGACCGCTTCTGCTGCTTTACGGTATCGCGCTCCCGATTGCG 1140
QY 1141 AGGCGATCGGCTTCTATCGGCTTCTGACGAGTTCCTTCTGAGTTAAACAGACCAACG 1200
Db 1141 AGGCGATCGGCTTCTATCGGCTTCTGACGAGTTCCTTCTGAGTTAAACAGACCAACG 1200
QY 1201 GTTTCCTCTAGCGGGATCAATTCGCGCCCTCTCCCTCCCGCCCTTAAGCTTACTGCG 1260
Db 1201 GTTTCCTCTAGCGGGATCAATTCGCGCCCTCTCCCTCCCGCCCTTAAGCTTACTGCG 1260
QY 1261 CGAAGCGCTTGAATGAAGCGGCTGCTGCTATATGTTATATTTCCACCATATG 1320
Db 1261 CGAAGCGCTTGAATGAAGCGGCTGCTGCTATATGTTATATTTCCACCATATG 1320
QY 1321 CCGTCTTTTGGCAATGTAGGCGCCGGAACCTGCGCCCTCTCTTCTGACGAGCATTCCT 1380
Db 1321 CCGTCTTTTGGCAATGTAGGCGCCGGAACCTGCGCCCTCTCTTCTGACGAGCATTCCT 1380
QY 1381 AGGGGTCTTTCCTCTCGCAAGGAATGCAAGGTCTGTTGAATGCTGTTGAAGGAGCA 1440
Db 1381 AGGGGTCTTTCCTCTCGCAAGGAATGCAAGGTCTGTTGAATGCTGTTGAAGGAGCA 1440
QY 1441 GTTCTCTGGAAGCTTCTTGAAGACAAACACGCTCTGTAGCGACCTTTGCGAGCAGCG 1500
Db 1441 GTTCTCTGGAAGCTTCTTGAAGACAAACACGCTCTGTAGCGACCTTTGCGAGCAGCG 1500
QY 1501 AACCCCCACCTTGGGACAGTGCCTCTGGGCAAAAGCCAGCTGTATAGATACCT 1560
Db 1501 AACCCCCACCTTGGGACAGTGCCTCTGGGCAAAAGCCAGCTGTATAGATACCT 1560
QY 1561 GCAAGGGGCAACACCCAGTGCCACGTTGTGAGTTGATAGTTGTTGAAAGAGTCAAA 1620
Db 1561 GCAAGGGGCAACACCCAGTGCCACGTTGTGAGTTGATAGTTGTTGAAAGAGTCAAA 1620
QY 1621 TGGCTCTCTCAAGGATTAACAAAGGGGCTGAAGGATGCCAGAGGTACCCCATTTG 1680
Db 1621 TGGCTCTCTCAAGGATTAACAAAGGGGCTGAAGGATGCCAGAGGTACCCCATTTG 1680
QY 1681 ATGGGATCTGATCTGGGCTCGGTGCAATGCTTTTACATGTTTGTAGTGGAGGTAAAA 1740
Db 1681 ATGGGATCTGATCTGGGCTCGGTGCAATGCTTTTACATGTTTGTAGTGGAGGTAAAA 1740
QY 1741 AACGCTTAGGCCCCCGGACCAACCGGGGAGCTGGTTCCTTTGAAAAACAGGATATACC 1800
Db 1741 AACGCTTAGGCCCCCGGACCAACCGGGGAGCTGGTTCCTTTGAAAAACAGGATATACC 1800
QY 1801 ATGGCGCTTATACGGCTACTCCCAACAGACGAGGCGCTACTTGGCTGCATCATCACT 1860

Db 1801 ATGGCGCTTATACGGCTACTCCCAACAGACGCGAGGCGCTACTTGGCTGCATCATCACT 1860
QY 1861 AGCCTCACAGGCGCGGACAGGAACAGAGTCAGGTCCAGGGGAGGTCCAGGTGCTCCACCGCA 1920
Db 1861 AGCCTCACAGGCGCGGACAGGAACAGAGTCAGGTCCAGGGGAGGTCCAGGTGCTCCACCGCA 1920
QY 1921 ACACAATCTTCTGGCGACCTGCTCAATGAGCGCTGTGTGGACTGTCTATCATGCTGCC 1980
Db 1921 ACACAATCTTCTGGCGACCTGCTCAATGAGCGCTGTGTGGACTGTCTATCATGCTGCC 1980
QY 1981 GGTCTAAAGAGCCCTTGGCGGCGCCAAAGGGCCCAATACCCAAATGTACACCAATGTGGAC 2040
Db 1981 GGTCTAAAGAGCCCTTGGCGGCGCCAAAGGGCCCAATACCCAAATGTACACCAATGTGGAC 2040
QY 2041 CAGGACCTCGCTCGGCTGGCAAGCGCCCCCGGGCGGCTTCTTGGACACCATGCACTGCG 2100
Db 2041 CAGGACCTCGCTCGGCTGGCAAGCGCCCCCGGGCGGCTTCTTGGACACCATGCACTGCG 2100
QY 2101 GGCAGCTCGGACCTTTACTTGGTCAAGGCGCATGCGGATGTCAATTCGGTGC CGCGGG 2160
Db 2101 GGCAGCTCGGACCTTTACTTGGTCAAGGCGCATGCGGATGTCAATTCGGTGC CGCGGG 2160
QY 2161 GGCAGACAGCGGGGAGCCTACTCTCCCGAGGCGGCTTCTCTACTTTGAAGGGCTCTTCG 2220
Db 2161 GGCAGACAGCGGGGAGCCTACTCTCCCGAGGCGGCTTCTCTACTTTGAAGGGCTCTTCG 2220
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Db 2221 GGGGCTCCACTGCTCTGCGGCGACGCTGTGGGCGATCTTCCGGGCTGCGGCTGTC 2280
QY 2281 ACCGAGGGGTGCGAAGCGGTGGAATTTGTATCCCGTTCAGTCTATGGAACACCACTATG 2340
Db 2281 ACCGAGGGGTGCGAAGCGGTGGAATTTGTATCCCGTTCAGTCTATGGAACACCACTATG 2340
QY 2341 CGGTCCCGGCTCTACGAGCAACTGTCCTCCCTCGGCGGCTACCGGACATTCACAGGTG 2400
Db 2341 CGGTCCCGGCTCTACGAGCAACTGTCCTCCCTCGGCGGCTACCGGACATTCACAGGTG 2400
QY 2401 GCCCATCTACACGCCCTCTACTGTAGCGGCAAGAGCACTAAGGTGCGGCTGGTATGCA 2460
Db 2401 GCCCATCTACACGCCCTCTACTGTAGCGGCAAGAGCACTAAGGTGCGGCTGGTATGCA 2460
QY 2461 GCCAAGGTATAGGTGCTTCTTAAACCGGCTCGGCGGCGGCGGCTAGGTTTCGGG 2520
Db 2461 GCCAAGGTATAGGTGCTTCTTAAACCGGCTCGGCGGCGGCGGCTAGGTTTCGGG 2520
QY 2521 GGTATATCTTAAAGCAGATGCTATCGACCTTAACATCAGAACCGGGGTAAAGCAATC 2580
Db 2521 GGTATATCTTAAAGCAGATGCTATCGACCTTAACATCAGAACCGGGGTAAAGCAATC 2580
QY 2581 ACCAGGGTGCCCGGCTACGCTACTCCACTATGCAAGTTCCTTTCGCGACCGGTGCTTCG 2640
Db 2581 ACCAGGGTGCCCGGCTACGCTACTCCACTATGCAAGTTCCTTTCGCGACCGGTGCTTCG 2640
QY 2641 TCTGGGGCGCTATGACATATAATATGATGAGTGCACCTCAACTGACTCGACCACT 2700
Db 2641 TCTGGGGCGCTATGACATATAATATGATGAGTGCACCTCAACTGACTCGACCACT 2700
QY 2701 ATCTTGGGCGCTCGGACAGTCTTCCGACCAAGCGGAGCGGCTGGAGCGGCTCGCTCGTG 2760
Db 2701 ATCTTGGGCGCTCGGACAGTCTTCCGACCAAGCGGAGCGGCTGGAGCGGCTCGCTCGTG 2760
QY 2761 CTCGCCACCGCTACCGCTTCCGGATCGGTGCGGCGGCTGCGGCGGCTGCGGCGGCTGCG 2820
Db 2761 CTCGCCACCGCTACCGCTTCCGGATCGGTGCGGCGGCTGCGGCGGCTGCGGCGGCTGCG 2820
QY 2821 GCTCTGTCCAGCACTGGAGAAATCCCTTTTATGGCAAGGCGCATCCCATCGAGACCAATC 2880
Db 2821 GCTCTGTCCAGCACTGGAGAAATCCCTTTTATGGCAAGGCGCATCCCATCGAGACCAATC 2880
QY 2881 AAGGGGGGAGGCGGCTTCTTCTGCGCATTCAGAGAAATGTGATGAGCTCGCGCG 2940

QY	5101	GATGGGTGCGGTGTCACAGGTACCGTCCAGCGTGCAAAACCCCTCCTACGGGAGGATC	5160	Db	6181	GTGCTCAAGGAGATGAAGCGAAGCGCTCCACAGTTAAGGCTTAAACTTCTATCCCGTGGAG	6240
Db	5101	GATGGGTGCGGTGTCACAGGTACCGTCCAGCGTGCAAAACCCCTCCTACGGGAGGATC	5160	QY	6241	GAAGCCTGTAAAGCTGACGCCCCACATTCGGGCCACATCTAAATTTGGCTATCGGGCAAG	6300
QY	5161	ACATTCCTGGTGGGTGCTCAATCAATACCTGTTGGTTCACAGCTCCATTCGAGCCCGAA	5220	Db	6241	GAAGCCTGTAAAGCTGACGCCCCACATTCGGGCCACATCTAAATTTGGCTATCGGGCAAG	6300
Db	5161	ACATTCCTGGTGGGTGCTCAATCAATACCTGTTGGTTCACAGCTCCATTCGAGCCCGAA	5220	QY	6301	GACGTCCGGAACCTATTCAGCAAGGCGGTAAACCACTCCGCTCCGTGTGGAGGACTTG	6360
QY	5221	CCGACGTAGTAGTCTCACTTCCATGTCTACCGACCCCTCCCACTTACGCGGAGAGC	5280	Db	6301	GACGTCCGGAACCTATTCAGCAAGGCGGTAAACCACTCCGCTCCGTGTGGAGGACTTG	6360
Db	5221	CCGACGTAGTAGTCTCACTTCCATGTCTACCGACCCCTCCCACTTACGCGGAGAGC	5280	QY	6361	CTGGAAGACATGAGACACCAATTCGACACCACTATCGGCAAAATAATGAGTTTCTGC	6420
QY	5281	GCTAAGCGTAGCTGGCCAGGGGATCTCCCTCTCTTGGCCAGCTCATCAGCTAGCCAG	5340	Db	6361	CTGGAAGACATGAGACACCAATTCGACACCACTATCGGCAAAATAATGAGTTTCTGC	6420
Db	5281	GCTAAGCGTAGCTGGCCAGGGGATCTCCCTCTCTTGGCCAGCTCATCAGCTAGCCAG	5340	QY	6421	GTCCAAACAGAGAAGGGGGCGCAAGCCAGCTCGCTTATCGTATTCGCCAGATTGGGG	6480
QY	5341	CTGTCTGGCCCTTCTTGAAGCAACATGCACTACCGTCTATGCTCCCGGACGCTGAC	5400	Db	6421	GTCCAAACAGAGAAGGGGGCGCAAGCCAGCTCGCTTATCGTATTCGCCAGATTGGGG	6480
Db	5341	CTGTCTGGCCCTTCTTGAAGCAACATGCACTACCGTCTATGCTCCCGGACGCTGAC	5400	QY	6481	GTTCTGTGTGCGAGAAATGGCCCTTTACGATGTGTCTCCACCTCCCTCAGGCCGTG	6540
QY	5401	CTCATCGAGGCCAACCCTCTGTGGCGCAGGAGATGGCGGGAAACATCACCCGGTGGAG	5460	Db	6481	GTTCTGTGTGCGAGAAATGGCCCTTTACGATGTGTCTCCACCTCCCTCAGGCCGTG	6540
Db	5401	CTCATCGAGGCCAACCCTCTGTGGCGCAGGAGATGGCGGGAAACATCACCCGGTGGAG	5460	QY	6541	ATGGCTCTTCTATACGATTCCTCAATATCTCTCTGGAAGGGGTGCGAGTTCTCTGTAAT	6600
QY	5461	TCGAAATTAAGGTAGTAAATTTTGGACTCTTTTCGAGCGCTCCAAAGCGGAGGATGAG	5520	Db	6541	ATGGCTCTTCTATACGATTCCTCAATATCTCTCTGGAAGGGGTGCGAGTTCTCTGTAAT	6600
Db	5461	TCGAAATTAAGGTAGTAAATTTTGGACTCTTTTCGAGCGCTCCAAAGCGGAGGATGAG	5520	QY	6601	GCCTGGAAGCGAGAAATGCCCTATGGGCTTCGCATATGACACCCCTCTGTTGACTCA	6660
QY	5521	AGGGAAGTATCCGTTCCGGCGGAGATCTCGGAGGTCGAGGAATTCCTTCGAGCGATG	5580	Db	6601	GCCTGGAAGCGAGAAATGCCCTATGGGCTTCGCATATGACACCCCTCTGTTGACTCA	6660
Db	5521	AGGGAAGTATCCGTTCCGGCGGAGATCTCGGAGGTCGAGGAATTCCTTCGAGCGATG	5580	QY	6661	ACGGTCACTGAGAAATGACATCCGTTGTGAGGAGTCAATCTACCAATCTGTTGACTGGCC	6720
QY	5581	CCCATATGGGCAACCGCGGATTAACACCTCCACTGTTAGAGTCTTGGAGGACCCGGAC	5640	Db	6661	ACGGTCACTGAGAAATGACATCCGTTGTGAGGAGTCAATCTACCAATCTGTTGACTGGCC	6720
Db	5581	CCCATATGGGCAACCGCGGATTAACACCTCCACTGTTAGAGTCTTGGAGGACCCGGAC	5640	QY	6721	CCGGAAGCCAGACAGGCCATTAAGGTCGCTCACAGAGCGGCTTTACATCGGGGCCCCCTG	6780
QY	5641	TACGTCCTCCAGTGTACAGGGGTGTCATGCGGCTCCCAAGGCCCTCCGATACCA	5700	Db	6721	CCGGAAGCCAGACAGGCCATTAAGGTCGCTCACAGAGCGGCTTTACATCGGGGCCCCCTG	6780
Db	5641	TACGTCCTCCAGTGTACAGGGGTGTCATGCGGCTCCCAAGGCCCTCCGATACCA	5700	QY	6781	ACTAATCTTAAAGGCGAGAACTCGCGGTATCGCGGTGCGCGCGAGCGGTGACTGAGC	6840
QY	5701	CCTCCAGGAGGAGGAGCGGTTGCTGTCAGATCTACCGTGTCTTCTGCTTGGGG	5760	Db	6781	ACTAATCTTAAAGGCGAGAACTCGCGGTATCGCGGTGCGCGCGAGCGGTGACTGAGC	6840
Db	5701	CCTCCAGGAGGAGGAGCGGTTGCTGTCAGATCTACCGTGTCTTCTGCTTGGGG	5760	QY	6841	ACCAGTCCGGAATACCTCTCACTGTTACTTGAAGCGCGCTGCGCGCTGCTGAGTGGC	6900
QY	5761	GAGTCCGCAACAAGACCTTCGSCAGCTCCGATCGTGGCGTCCAGCGGACCGCA	5820	Db	6841	ACCAGTCCGGAATACCTCTCACTGTTACTTGAAGCGCGCTGCGCGCTGCTGAGTGGC	6900
Db	5761	GAGTCCGCAACAAGACCTTCGSCAGCTCCGATCGTGGCGTCCAGCGGACCGCA	5820	QY	6901	AAAGTCCAGGACTGACGATGCTCGTATCGGAGACGACTTGTGTTATCTGTGAAAGC	6960
QY	5821	ACGGCTCTCTGACAGCGCTCCGAGACGCGGATCCGAGCGCGGATCCGACGTTGAGTCTATC	5880	Db	6901	AAAGTCCAGGACTGACGATGCTCGTATCGGAGACGACTTGTGTTATCTGTGAAAGC	6960
Db	5821	ACGGCTCTCTGACAGCGCTCCGAGACGCGGATCCGAGCGCGGATCCGACGTTGAGTCTATC	5880	QY	6961	GGGGGACCCAAAGAGACGAGCGGAGCTTACGGGCTTACAGGAGCTATGACTAGATAC	7020
QY	5881	TCCTCCATGCCCCCTTGGAGGAGCGCGGATCCCGATCTCAGCGCGGCTTGG	5940	Db	6961	GGGGGACCCAAAGAGACGAGCGGAGCTTACGGGCTTACAGGAGCTATGACTAGATAC	7020
Db	5881	TCCTCCATGCCCCCTTGGAGGAGCGCGGATCCCGATCTCAGCGCGGCTTGG	5940	QY	7021	TCCTCCATGTTGTCAGTCCGCGCATGTCATCTGCAAAAGGGTGTACTATCTCACCCTG	7080
QY	5941	TCTACCGTAAGCGAGGAGCTAGTGAAGACGTCGTCGTCGTCGATCTCAGCGACGGCTTGG	6000	Db	7021	TCCTCCATGTTGTCAGTCCGCGCATGTCATCTGCAAAAGGGTGTACTATCTCACCCTG	7080
Db	5941	TCTACCGTAAGCGAGGAGCTAGTGAAGACGTCGTCGTCGTCGATCTCAGCGACGGCTTGG	6000	QY	7081	TCCTCCATGTTGTCAGTCCGCGCATGTCATCTGCAAAAGGGTGTACTATCTCACCCTG	7140
QY	6001	ACAGCGCCCTGATCAGCGCATGCGCTGGGAGGAAACCAAGCTGCCATCAATGACTG	6060	Db	7081	TCCTCCATGTTGTCAGTCCGCGCATGTCATCTGCAAAAGGGTGTACTATCTCACCCTG	7140
Db	6001	ACAGCGCCCTGATCAGCGCATGCGCTGGGAGGAAACCAAGCTGCCATCAATGACTG	6060	QY	7141	GACCCCAACCCCTTGGCGGCGCTGCGGAGAGCTAGACACACTCCAGTCAAT	7200
QY	6061	AGCAACTCTTGTCCGTCACCAACCTGTTGTCATGTCATGTCATGTCAGCGCAAGC	6120	Db	7141	GACCCCAACCCCTTGGCGGCGCTGCGGAGAGCTAGACACACTCCAGTCAAT	7200
Db	6061	AGCAACTCTTGTCCGTCACCAACCTGTTGTCATGTCATGTCATGTCAGCGCAAGC	6120	QY	7201	TCCTGGCTAGCAACATCATCATGTCATGTCGCGCCCTTGTGGCAAGGATGATCTCTGATG	7260
QY	6121	CTGGCGAGAGAGGTCACCTTTGACAGACTGACAGTCCCTGGAGCGACCTACCGGAC	6180	Db	7201	TCCTGGCTAGCAACATCATCATGTCATGTCGCGCCCTTGTGGCAAGGATGATCTCTGATG	7260
Db	6121	CTGGCGAGAGAGGTCACCTTTGACAGACTGACAGTCCCTGGAGCGACCTACCGGAC	6180	QY	7261	ACTCATTTCTTCTCCATCTTCTAGCTCAGGAAACCTTGAAGGCTTAACTTCTATCCGTGGAG	7320
QY	6181	GTGCTCAAGGAGATGAAGCGGAGCGCTCCACAGTTAAGGCTTAACTTCTATCCGTGGAG	6240				

Db 7261 ACTCATTTCTTCCATCTCTTAGCTCAGGAAACAATCTGAAAGCCCTAGATTCTCAG 7320
 QY 7321 ATCTAGCGGCGCTTGTACTCCATTGAGCCACTTGTACTCTCAGATCAATCAACGACTC 7380
 Db 7321 ATCTAGCGGCGCTTGTACTCCATTGAGCCACTTGTACTCTCAGATCAATCAACGACTC 7380
 QY 7381 CATGGCCTTAGCGCAATTTTCACTCCATAGTACTCTCCAGTGAGATCAATAGGGTGGCT 7440
 Db 7381 CATGGCCTTAGCGCAATTTTCACTCCATAGTACTCTCCAGTGAGATCAATAGGGTGGCT 7440
 QY 7441 TCATGCTCAGGAAACTTGGGCTACCGCTGCTGAGTCTGGAGACATCGGGCCAGAGT 7500
 Db 7441 TCATGCTCAGGAAACTTGGGCTACCGCTGCTGAGTCTGGAGACATCGGGCCAGAGT 7500
 QY 7501 GTCCGCGCTAGGCTACTGTCTCCAGGGGGAGGGCTGCTCACTTGTGGCAAGTACTCTTC 7560
 Db 7501 GTCCGCGCTAGGCTACTGTCTCCAGGGGGAGGGCTGCTCACTTGTGGCAAGTACTCTTC 7560
 QY 7561 AACTGGGCGAGTAAGGACCAAGCTCAACTCACTCCATCCCGCTGGCTCCAGTTGGAT 7620
 Db 7561 AACTGGGCGAGTAAGGACCAAGCTCAACTCACTCCATCCCGCTGGCTCCAGTTGGAT 7620
 QY 7621 TTATCCAGCTGGTTCGTTGCTGCTTACAGCGGGGAGACATATATCAAGCTGTCTCGT 7680
 Db 7621 TTATCCAGCTGGTTCGTTGCTGCTTACAGCGGGGAGACATATATCAAGCTGTCTCGT 7680
 QY 7681 GCGGACCCCGCTGGTTCATGTGTGCTTACTCTTCTGTAGGGGTAGGCACTAT 7740
 Db 7681 GCGGACCCCGCTGGTTCATGTGTGCTTACTCTTCTGTAGGGGTAGGCACTAT 7740
 QY 7741 CTACTCCCAACCGAGTAAGGAGGAGCTAAACACTCCAGGCAATAGGCCATCTCTTT 7800
 Db 7741 CTACTCCCAACCGAGTAAGGAGGAGCTAAACACTCCAGGCAATAGGCCATCTCTTT 7800
 QY 7801 TTTCCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7860
 Db 7801 TTTCCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7860
 QY 7861 TTTTCTCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 7920
 Db 7861 TTTTCTCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 7920
 QY 7921 TAGCTGTGAAGGCTCGTGAGCGGCTTGACTGAGAGAGTGTCTGATCTGCTCTCTGC 7980
 Db 7921 TAGCTGTGAAGGCTCGTGAGCGGCTTGACTGAGAGAGTGTCTGATCTGCTCTCTGC 7980
 QY 7981 AGATCAAGTACT 7992
 Db 7981 AGATCAAGTACT 7992

RESULT 4
 AD83762
 ID AD83762 standard; DNA; 10690 BP.
 XX
 AC AD83762;
 XX
 DT 01-JAN-2004 (first entry)
 XX pHVNeol7.wt plasmid containing an HCV bicistronic replicon.
 DE
 XX Hepatitis C virus; thiosemicarbazone; RHEPLISA; Ia; hepatitis C;
 KW 4-(Cinnamyl)oxybenzaldehyde thiosemicarbazone; RHEPLISA; Ia; hepatitis C;
 KW HCV replication system; bicistronic RNA replicon;
 KW neomycin phosphotransferase; human hepatoma cell line; Huh-7;
 KW neomycin sulphate; G418; pHVNeol7.wt; replicon 1377neo/NS3-3/wt.;
 KW hepatotropic; virucide; antiinflammatory; ds.
 XX
 OS Synthetic.
 OS Unidentified.
 OS Hepatitis C virus.
 XX
 FN US2003176503-A1.

XX 18-SRP-2003.
 XX 19-APR-2002; 2002US-00125920.
 XX 20-APR-2001; 2001US-0295195P.
 XX (ALTA/) ALTAMURA S.
 XX (KOCH/) KOCH U.
 XX Altamura S, Koch U;
 XX WPI; 2003-778475/73.
 XX Use of thiosemicarbazone compounds for e.g. treating and preventing
 XX hepatitis C or its related condition, and delaying the onset of hepatitis
 XX C or its related condition.
 XX Example 3; SEQ ID NO 1; 30pp; English.
 XX The invention discloses a method for the treatment and prevention of
 XX hepatitis C, or its related condition, which involves the administration
 XX of thiosemicarbazone compounds, or its salts. The inhibitory activity of
 XX 4-(cinnamyl)oxybenzaldehyde thiosemicarbazone was evaluated using
 XX RHEPLISA assay in a 96-well microplate format. The route of
 XX administration is oral, parenteral (e.g. subcutaneous, intravenous,
 XX intramuscular, intrasternal injection, or infusion), by inhalation spray
 XX or rectal. The use of the 35 compounds disclosed is specifically claimed,
 XX e.g. 4-(cinnamyl)oxybenzaldehyde thiosemicarbazone (Ia). The compounds
 XX are useful for treating and preventing hepatitis C or its related
 XX condition, delaying the onset of hepatitis C or its related condition and
 XX inhibiting replication of the hepatitis C virus. HCV replication
 XX inhibitors can be obtained using various techniques. Selection of cells
 XX capable of supporting HCV replication can be achieved using bicistronic
 XX RNA replicons expressing a selectable marker, the neomycin
 XX phosphotransferase. Transfection of these replicons in the human hepatoma
 XX cell line, Huh-7, followed by isolation of clones that support HCV
 XX sulphate (G418), permits the isolation of clones that support HCV
 XX replication. The sequence presented is the pHVNeol7.wt plasmid which
 XX contains the CDNA coding for an HCV bicistronic replicon identical to
 XX replicon 1377neo/NS3-3/wt.
 XX
 XX Sequence 10690 BP; 2334 A; 3045 C; 2908 G; 2403 T; 0 U; 0 Other;
 Query Match 99.9%; Score 7985.6; DB 9; Length 10690;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 7988; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 GCCAGCCCCCGATTGGGGGGGACACTCCACCATAGATCACTCCCTGTGAGGAATCTG 60
 Db 1 GCCAGCCCCCGATTGGGGGGGACACTCCACCATAGATCACTCCCTGTGAGGAATCTG 60
 QY 61 TCTTTCAGCAGAAAGCGTCTAGCCATGGGCTTAGTATGATGCTGTCGAGCCTCCAGGAC 120
 Db 61 TCTTTCAGCAGAAAGCGTCTAGCCATGGGCTTAGTATGATGCTGTCGAGCCTCCAGGAC 120
 QY 121 CCCCCCTCCCGGAGAGCCATAGTGTCTCGGAAACCGGTGATACACCGGAATTCGAC 180
 Db 121 CCCCCCTCCCGGAGAGCCATAGTGTCTCGGAAACCGGTGATACACCGGAATTCGAC 180
 QY 181 GAGACCGGTCTCTTCTTGGATCAACCCGCTCAATGCCCTGGAGATTGGCGCTGCCCCC 240
 Db 181 GAGACCGGTCTCTTCTTGGATCAACCCGCTCAATGCCCTGGAGATTGGCGCTGCCCCC 240
 QY 241 GCGAGACTGCTAGCCGAGTAGTGTGGGTGCGGAAAGCCCTTGTGTTACTGCTGATAGG 300
 Db 241 GCGAGACTGCTAGCCGAGTAGTGTGGGTGCGGAAAGCCCTTGTGTTACTGCTGATAGG 300
 QY 301 GTGCTTCGAGTGCCTCCGGGAGGTCTGTAGACCGTGCACCATGAGCAGCAATCTTAAC 360
 Db 301 GTGCTTCGAGTGCCTCCGGGAGGTCTGTAGACCGTGCACCATGAGCAGCAATCTTAAC 360

QY 361 CTCAAAGAAAACAAAGCGCGCCCATGATTGAACAAGATGGAATTGACGAGGTTCTC 420
Db |||||
QY 361 CTCAAAGAAAACAAAGCGCGCCCATGATTGAACAAGATGGAATTGACGAGGTTCTC 420
Db |||||
QY 421 CGGCGCTTGGGTGGAGAGGCTATTCCGCTATGACTGGGCAACAAGCAATTCGGCTGCT 480
Db |||||
QY 421 CGGCGCTTGGGTGGAGAGGCTATTCCGCTATGACTGGGCAACAAGCAATTCGGCTGCT 480
Db |||||
QY 481 CTGATGCCGCCGTGTTCGGGCTGTGAGCGACGGGCGCCCGTCTCTTTTGTGCAAGACG 540
Db |||||
QY 481 CTGATGCCGCCGTGTTCGGGCTGTGAGCGACGGGCGCCCGTCTCTTTTGTGCAAGACG 540
Db |||||
QY 541 ACCTGTCCGGTCCCTGAATGAATCTGAGGACGAGCGCGGCTATCGTGGCTGGCCA 600
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QY 541 ACCTGTCCGGTCCCTGAATGAATCTGAGGACGAGCGCGGCTATCGTGGCTGGCCA 600
Db |||||
QY 601 CGAGGGGCTTCCCTTGGCGAGCTGTCTGAGCGAGGCGGCTGCTGCTGCTGCTGCTGCT 660
Db |||||
QY 601 CGAGGGGCTTCCCTTGGCGAGCTGTCTGAGCGAGGCGGCTGCTGCTGCTGCTGCTGCT 660
Db |||||
QY 661 TGTATTGGGCAAGTGGCGGGCAGGATCTCTGTCTATCTCACTTGTCTCTCTCGCGAGA 720
Db |||||
QY 661 TGTATTGGGCAAGTGGCGGGCAGGATCTCTGTCTATCTCACTTGTCTCTCTCGCGAGA 720
Db |||||
QY 721 AAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCTATGCTGCTGCTGCTGCTGCTGCT 780
Db |||||
QY 721 AAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCTATGCTGCTGCTGCTGCTGCTGCT 780
Db |||||
QY 781 CATTCGACCAACCAAGCGAAACATCGCATCGAGCGAGCACTGCTGCTGCTGCTGCTGCTGCT 840
Db |||||
QY 781 CATTCGACCAACCAAGCGAAACATCGCATCGAGCGAGCACTGCTGCTGCTGCTGCTGCTGCT 840
Db |||||
QY 841 TTGTGATCAGGATGATCTGGAAGAGAGATCAGGGGCTCGCGCCAGCGCACTGCTGCTGCT 900
Db |||||
QY 841 TTGTGATCAGGATGATCTGGAAGAGAGATCAGGGGCTCGCGCCAGCGCACTGCTGCTGCT 900
Db |||||
QY 901 CAGGCTCAGGCGCGCATCGCGAAGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
Db |||||
QY 901 CAGGCTCAGGCGCGCATCGCGAAGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
Db |||||
QY 961 GCTTGCAGAAATCATGCTGGAATGCGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
Db |||||
QY 961 GCTTGCAGAAATCATGCTGGAATGCGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
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QY 1021 TGGGTGCGGACCGCTATCAGGACATAGCGTTGCTACCGCTGATATTGCTGGAAGGC 1080
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QY 1021 TGGGTGCGGACCGCTATCAGGACATAGCGTTGCTACCGCTGATATTGCTGGAAGGC 1080
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QY 1081 TTGGCGGCAATGGGCTGACCGCTTCTGCTGCTTACGGTATCGCGCTCCCGATTGCG 1140
Db |||||
QY 1081 TTGGCGGCAATGGGCTGACCGCTTCTGCTGCTTACGGTATCGCGCTCCCGATTGCG 1140
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QY 1141 AGCGCATCGCTTCTATCGCTTCTGAGAGTTCTTCTGAGTTTAAACAGACCAAGC 1200
Db |||||
QY 1141 AGCGCATCGCTTCTATCGCTTCTGAGAGTTCTTCTGAGTTTAAACAGACCAAGC 1200
Db |||||
QY 1201 GTTTCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCTTAACTGCTGCTGCTGCT 1260
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QY 1201 GTTTCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCTTAACTGCTGCTGCTGCT 1260
Db |||||
QY 1261 GGAAGCGCTTGAATAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
Db |||||
QY 1261 GGAAGCGCTTGAATAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
Db |||||
QY 1321 CGCTTTTGGCAATGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
Db |||||
QY 1321 CGCTTTTGGCAATGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
Db |||||
QY 1381 AGGGGTCTTCCCTCTCGCCAAAGGAATGCAAGGTCTGTTGAAATGCTGTAAGGAAGCA 1440
Db |||||
QY 1381 AGGGGTCTTCCCTCTCGCCAAAGGAATGCAAGGTCTGTTGAAATGCTGTAAGGAAGCA 1440
Db |||||
QY 1441 GTTCTCTGGAAGCTTCTTGAAGACAAACAAAGTCTGTAGCGACCTTTGCGAGCGCGG 1500
Db |||||

Db |||||
QY 1441 GTTCTCTGGAAGCTTCTTGAAGACAAACAAAGTCTGTAGCGACCTTTGCGAGCGCG 1500
Db |||||
QY 1501 AACCCCCACCTGGCGACAGGTGCTCTCGGCGCAAAAGCCACAGTGTATTAAGATACCT 1560
Db |||||
QY 1501 AACCCCCACCTGGCGACAGGTGCTCTCGGCGCAAAAGCCACAGTGTATTAAGATACCT 1560
Db |||||
QY 1561 GCAAGGCGGCAACACCCAGTGCACCTGTGTGAGTGTGATAGTTGTGGAAGAGTCAAA 1620
Db |||||
QY 1561 GCAAGGCGGCAACACCCAGTGCACCTGTGTGAGTGTGATAGTTGTGGAAGAGTCAAA 1620
Db |||||
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Db |||||
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Db |||||
QY 1681 ATGGATCTGATCTGGGCTCTGGTGCACATGCTTTACATGTTTGTGAGGTTAAAA 1740
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QY 1741 AACGTCAGGCTTGGGCTCTGGTGCACATGCTTTTCTTTGAAAAACAGATAATACC 1800
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QY 1741 AACGTCAGGCTTGGGCTCTGGTGCACATGCTTTTCTTTGAAAAACAGATAATACC 1800
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QY 1801 ATGGGCTTATTAGGCTTACTCCAAAGAGCGGCTTACTTGGCTGATCATCACT 1860
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QY 1861 AGCTCAGAGCGGCGACAGAACAGTGCAGAGGAGGTCCAGGTGGTCTCCACCGCA 1920
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QY 1861 AGCTCAGAGCGGCGACAGAACAGTGCAGAGGAGGTCCAGGTGGTCTCCACCGCA 1920
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QY 1921 ACACATCTTCTGGCGACTCGTCAATGGCGTGTGTGGAGTCTCTATCATGTTGCC 1980
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QY 1921 ACACATCTTCTGGCGACTCGTCAATGGCGTGTGTGGAGTCTCTATCATGTTGCC 1980
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QY 1981 GGCTCAAGACCTTGGCGGCTTGGCGGCTTGGCGGCTTGGCGGCTTGGCGGCTTGGCGGCT 2040
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QY 2041 CAGGACTCTGCTGGCTGGCAAGCGCCCGCGGCGGCTTCTTGACACCATGCACTGC 2100
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QY 2461 GCGCATCTACAGCGCTTACTGCTAGCGGCAAGAGCACTAAGGTCGCGGCTGCGTATGCA 2520
Db |||||
QY 2521 GCGTATGCTTGAAGGCACTGCTATGCAACCGCTTGAAGGCTTGAAGGCTTGAAGGCTTGAAGGCT 2580
Db |||||

Db	2521	GCCTATATGTCTAAGGCACATGATATCGACCCCTAAATCATCAGAACCGGGTAAAGACCATC	2580	3661	ATGGCATCATGTCTGGCTGACCTGGAGGTGTCACAGACACCTGGGTGCTGTAGGCGGA	3720
Qy	2581	ACCACGGGTCCCCCACTACCTACTCCACCTATGCGAAGTTTCTTGCCGACGGTGGTTC	2640	3661	ATGGCATCATGTCTGGCTGACCTGGAGGTGTCACAGACACCTGGGTGCTGTAGGCGGA	3720
Db	2581	ACCACGGGTCCCCCACTACCTACTCCACCTATGCGAAGTTTCTTGCCGACGGTGGTTC	2640	3721	GTCTAGCAGCTCTGGCCGGGTATTGCTGACACAGGACGCTGCTCATTTGGGCGAG	3780
Qy	2641	TCTGGGGCGCCTATGACATCAATAATGATGATGAGTGCCACTCAACTGACTGCACCACT	2700	3721	GTCTAGCAGCTCTGGCCGGGTATTGCTGACACAGGACGCTGCTCATTTGGGCGAG	3780
Db	2641	TCTGGGGCGCCTATGACATCAATAATGATGATGAGTGCCACTCAACTGACTGCACCACT	2700	3781	ATCATCTTGTCCGGAAGCCCGCCATCATTTCCCGACAGGGAAGTCTTTTACCGGAGTTC	3840
Qy	2701	ATCTGGGATCCGACAGTCTCTGGACCAAGCGAGACGGTGGAGCGCACTCTGCTGTG	2760	3781	ATCATCTTGTCCGGAAGCCCGCCATCATTTCCCGACAGGGAAGTCTTTTACCGGAGTTC	3840
Db	2701	ATCTGGGATCCGACAGTCTCTGGACCAAGCGAGACGGTGGAGCGCACTCTGCTGTG	2760	3841	GATGAGATGGAAGAGTCTGCTCATCTCTCTTACATCGAAGAGGAATTCAGCTCGCC	3900
Qy	2761	CTGCCACCGCTAGCCCTCCGGGATCGGTCAACCGTGCCACATCCAAACATCGAGGAGTG	2820	3841	GATGAGATGGAAGAGTCTGCTCATCTCTCTTACATCGAAGAGGAATTCAGCTCGCC	3900
Db	2761	CTGCCACCGCTAGCCCTCCGGGATCGGTCAACCGTGCCACATCCAAACATCGAGGAGTG	2820	3901	GAAACAATTCAAACAGAGGCAATCGGGTCTGCAACAGCCACCAAGCAGCGAGGCT	3960
Qy	2821	GCTCTGTCAGACCTGGAGAAATCCCTTTTATGGCAAGCCATCCCATCGAGACCATC	2880	3901	GAAACAATTCAAACAGAGGCAATCGGGTCTGCAACAGCCACCAAGCAGCGAGGCT	3960
Db	2821	GCTCTGTCAGACCTGGAGAAATCCCTTTTATGGCAAGCCATCCCATCGAGACCATC	2880	3961	GCTGCTCCGCTGGTGAATCCAGTGGCGGACCTCTCGAAGCCTTTCTGGGCGAAGATATG	4020
Qy	2881	AAGGGGGGGGACCTCACTTTTCTGCCATTCGAAGAAATGTGATGAGTCTGCCGCG	2940	3961	GCTGCTCCGCTGGTGAATCCAGTGGCGGACCTCTCGAAGCCTTTCTGGGCGAAGATATG	4020
Db	2881	AAGGGGGGGGACCTCACTTTTCTGCCATTCGAAGAAATGTGATGAGTCTGCCGCG	2940	4021	TGGAAATTTTCATCAGCGGATACAATATTTAGCAGGCTTTGCTCCTCTGGCAACCC	4080
Qy	2941	AAGTGTCTCCGCTCGGACTCAATGCTGTAGCATATTACCGGGGCTTGATGATCCGTC	3000	4021	TGGAAATTTTCATCAGCGGATACAATATTTAGCAGGCTTTGCTCCTCTGGCAACCC	4080
Db	2941	AAGTGTCTCCGCTCGGACTCAATGCTGTAGCATATTACCGGGGCTTGATGATCCGTC	3000	4081	GCGATAGCATCACTGATGGCATTCACAGCCCTATCAGCCGCTCTCACACCCCAACAT	4140
Qy	3001	ATACCAACTAGCGGAGAGTGATGCTGTAGCAACGAGCGCTCTAATGACGGGCTTTACC	3060	4081	GCGATAGCATCACTGATGGCATTCACAGCCCTATCAGCCGCTCTCACACCCCAACAT	4140
Db	3001	ATACCAACTAGCGGAGAGTGATGCTGTAGCAACGAGCGCTCTAATGACGGGCTTTACC	3060	4141	ACCCTCTCTTTTAAACATCTGGGGGATGGGTGGCGCCCAACTTCTCTCCAGCGCT	4200
Qy	3061	GGCGATTTGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	3120	4141	ACCCTCTCTTTTAAACATCTGGGGGATGGGTGGCGCCCAACTTCTCTCCAGCGCT	4200
Db	3061	GGCGATTTGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	3120	4201	GCTTCTGCTTTCTAGGCGCGCATTCGCTGAGCGGCTTTGGCAGCATAGGCTTTGG	4260
Qy	3121	CTGGACCCGACCTTACCACTTACGACGACGCGGTGCCAAGACGCGGTGTCAAGCTGT	3180	4201	GCTTCTGCTTTCTAGGCGCGCATTCGCTGAGCGGCTTTGGCAGCATAGGCTTTGG	4260
Db	3121	CTGGACCCGACCTTACCACTTACGACGACGCGGTGCCAAGACGCGGTGTCAAGCTGT	3180	4261	AAAGTGTCTTGTGATATTTTGGCAGTATGAGCAGGCGCTGCGAGCGGCTCTGCTG	4320
Qy	3181	CAGCGCGAGGAGGAGTCTGATGAGGAGGAGTCTGATGAGGAGGAGTCTGATGAGGAG	3240	4261	AAAGTGTCTTGTGATATTTTGGCAGTATGAGCAGGCGCTGCGAGCGGCTCTGCTG	4320
Db	3181	CAGCGCGAGGAGGAGTCTGATGAGGAGGAGTCTGATGAGGAGGAGTCTGATGAGGAG	3240	4321	TTTAAAGTCTATGAGCGCGGATGCTCTCACCGAGGACCTGCTTAACTCTCTCTGCT	4380
Qy	3241	GAAAGCCCTCTGGGCAATGTTCTGATTTCTGCTGAGTGTCTGAGCGGCTGT	3300	4321	TTTAAAGTCTATGAGCGCGGATGCTCTCACCGAGGACCTGCTTAACTCTCTCTGCT	4380
Db	3241	GAAAGCCCTCTGGGCAATGTTCTGATTTCTGCTGAGTGTCTGAGCGGCTGT	3300	4381	ATCTCTCTCCCTGGCGCCCTAGTCTGCTGGGCTGCTGCGCAGCGATCTGCTGCGCAC	4440
Qy	3301	GCTTGTGATGAGTCTACGCGCGCGAGACCTCAGTTAGTTAGTTAGTTAGTTAGTTAG	3360	4381	ATCTCTCTCCCTGGCGCCCTAGTCTGCTGGGCTGCTGCGCAGCGATCTGCTGCGCAC	4440
Db	3301	GCTTGTGATGAGTCTACGCGCGCGAGACCTCAGTTAGTTAGTTAGTTAGTTAGTTAG	3360	4441	GTGGGCGCAGGAGGAGGAGGCTGTGAGTGAACCGGCTGATAGGCTTCTGCTTCCGCG	4500
Qy	3361	CGAGGTTGCGGCTGCGAGGACCATCTGGAGTCTGGAGAGCGCTTTTACAGGCTTC	3420	4441	GTGGGCGCAGGAGGAGGAGGCTGTGAGTGAACCGGCTGATAGGCTTCTGCTTCCGCG	4500
Db	3361	CGAGGTTGCGGCTGCGAGGACCATCTGGAGTCTGGAGAGCGCTTTTACAGGCTTC	3420	4501	GGTAAACCAAGTCTCTCCCGCAGCATATGTCCTGAGAGCGACGCTGAGCAGCGTGTCACT	4560
Qy	3421	ACCACATAGACGCCCATTTCTGTCCAGACTAAGCAGGACGAGAGCAACTTCCCTAC	3480	4501	GGTAAACCAAGTCTCTCCCGCAGCATATGTCCTGAGAGCGACGCTGAGCAGCGTGTCACT	4560
Db	3421	ACCACATAGACGCCCATTTCTGTCCAGACTAAGCAGGACGAGAGCAACTTCCCTAC	3480	4561	CAGATCTCTCTAGTCTTACCATCTCAGCTCTGTAAGAGGCTTACCAAGTGTATGATGC	4620
Qy	3481	CTGTTAGCATACAGGCTACGGTGTGCGCAGGCTCAGGCTCCACCTCCATCTGTTGAG	3540	4561	CAGATCTCTCTAGTCTTACCATCTCAGCTCTGTAAGAGGCTTACCAAGTGTATGATGC	4620
Db	3481	CTGTTAGCATACAGGCTACGGTGTGCGCAGGCTCAGGCTCCACCTCCATCTGTTGAG	3540	4621	GAGGACTGCTCCAGCGCATCTCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	4680
Qy	3541	CAAAATGGAAGTGTCTCATACGGCTAAAGCTACGCTGACGCGGCAACGCCCCCTGCT	3600	4621	GAGGACTGCTCCAGCGCATCTCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	4680
Db	3541	CAAAATGGAAGTGTCTCATACGGCTAAAGCTACGCTGACGCGGCAACGCCCCCTGCT	3600	4681	ACGGTGTGATGATTTTCAAGACCTGCTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGT	4740
Qy	3601	TATAGGCTGGAGCGGTTCAAAACGAGGTTACTACCAACACACACACACACACACACAC	3660	4681	ACGGTGTGATGATTTTCAAGACCTGCTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGT	4740
Db	3601	TATAGGCTGGAGCGGTTCAAAACGAGGTTACTACCAACACACACACACACACACACAC	3660			

Db 6901 AAGCTCCAGGACTGCGAGATGCTGCTATGCGGAGACGACCTTGTGTTATCTGTGAAGC 6960
QY 6961 GCGGGACCCCAAGAGGACGAGGCGAGCTTACGGGCTTTCAGGAGGCTATGACTAGATAC 7020
Db 6961 GCGGGACCCCAAGAGGACGAGGCGAGCTTACGGGCTTTCAGGAGGCTATGACTAGATAC 7020
QY 7021 TCTGCCCCCTCGGGACCCGCGCAACACGAGATACGACTTGGAGTTGATAACATCATGC 7080
Db 7021 TCTGCCCCCTCGGGACCCGCGCAACACGAGATACGACTTGGAGTTGATAACATCATGC 7080
QY 7081 TCCTCCAAATGTCAGTCGCGCAGATGCTCTGCAAAAGGGTGTACTATCTCACCGGT 7140
Db 7081 TCCTCCAAATGTCAGTCGCGCAGATGCTCTGCAAAAGGGTGTACTATCTCACCGGT 7140
QY 7141 GACCCACACCCCTTTCGCGGCTGCTGCGGAGACAGCTAGACACATCTCCAGTCAAT 7200
Db 7141 GACCCACACCCCTTTCGCGGCTGCTGCGGAGACAGCTAGACACATCTCCAGTCAAT 7200
QY 7201 TCCTGGCTAGCAACATCATGATGATGCGGCTGCTGCGGAGACAGCTAGATCTGATG 7260
Db 7201 TCCTGGCTAGCAACATCATGATGATGCGGCTGCTGCGGAGACAGCTAGATCTGATG 7260
QY 7261 ACTGATTTCTTCTCCATCTTCTAGCTCAGGAACAACTTGAAGAGCCCTAGATTTGTCAG 7320
Db 7261 ACTGATTTCTTCTCCATCTTCTAGCTCAGGAACAACTTGAAGAGCCCTAGATTTGTCAG 7320
QY 7321 ATCTACGGGCTGTTACTTCCATTCAGGACCTTGACCTACCTCAGATCATTCAGACTC 7380
Db 7321 ATCTACGGGCTGTTACTTCCATTCAGGACCTTGACCTACCTCAGATCATTCAGACTC 7380
QY 7381 CATGCGCTTAGCGATTTTCACTCCTAGTACTTCCAGGTGAGATCAATAGGTTGGCT 7440
Db 7381 CATGCGCTTAGCGATTTTCACTCCTAGTACTTCCAGGTGAGATCAATAGGTTGGCT 7440
QY 7441 TCATGCTCAGAACTTGGGTACCGCTTTCGAGTCTGAGACATCGGCGCAGACT 7500
Db 7441 TCATGCTCAGAACTTGGGTACCGCTTTCGAGTCTGAGACATCGGCGCAGACT 7500
QY 7501 GTCCGGCTAGGCTACTGTCAGGAGGAGGCTGCCACTTGTGGCAAGTACTCTTC 7560
Db 7501 GTCCGGCTAGGCTACTGTCAGGAGGAGGCTGCCACTTGTGGCAAGTACTCTTC 7560
QY 7561 AACTGGGCTAGTAAAGACCAAGCTCACTCCTACCTCCGCTCGTCCAGTTGGAT 7620
Db 7561 AACTGGGCTAGTAAAGACCAAGCTCACTCCTACCTCCGCTCGTCCAGTTGGAT 7620
QY 7621 TATTCAGTGTGCTGCTGCTTACAGCGGGGAGACATATACAGCCCTGTCTCGT 7680
Db 7621 TATTCAGTGTGCTGCTGCTTACAGCGGGGAGACATATACAGCCCTGTCTCGT 7680
QY 7681 GCGCGACCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 7740
Db 7681 GCGCGACCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 7740
QY 7741 CTACTCCCAACCGATGACGGGAGTAACTCCAGGCGCAATAGGCCATCTGTTTT 7800
Db 7741 CTACTCCCAACCGATGACGGGAGTAACTCCAGGCGCAATAGGCCATCTGTTTT 7800
QY 7801 TTTTCCCTTT 7860
Db 7801 TTTTCCCTTT 7860
QY 7861 TTTTTCCTTT 7920
Db 7861 TTTTTCCTTT 7920
QY 7921 TAGCTGTGAAGGTCGCTGAGCCGCTTACTGACGAGAGTCTGATCTAGTCCCTCTCTGC 7980
Db 7921 TAGCTGTGAAGGTCGCTGAGCCGCTTACTGACGAGAGTCTGATCTAGTCCCTCTCTGC 7980
QY 7981 AGATCAAGTACT 7992
Db 7981 AGATCAAGTACT 7992

RESULT 5

AA47281

ID AAL47281 standard; DNA; 7992 BP.

XX

AC AAL47281;

XX

DT 30-AUG-2002 (first entry)

XX

Hepatitis C virus sub-genomic replicon recombinant clone HCV24.

DB

Hepatitis; HCV; core-neo; NS3 proteinase/helicase; vaccine; diagnosis; virucide; hepatotropic; gene therapy; anti-viral; gene; ds.

XX

OS Hepatitis C virus.

XX

PN WO200238793-A2.

XX

PD 16-MAY-2002.

XX

PF 02-NOV-2001; 2001WO-US046350.

XX

PR 07-NOV-2000; 2000US-0245866P.

XX

PA (ANAD-) ANADYS PHARM INC.

XX

PI Bichko V;

XX

DR WPI; 2002-490082/52.

XX

Novel nucleic acid encoding replication competent recombinant hepatitis C virus genome useful for screening anti-hepatitis C virus therapeutics and for vaccine development.

XX

Claim 11; Page 70-75; 85pp; English.

PS

The present invention provides protein and coding sequences from Hepatitis C virus (HCV), comprising all or part of the HCV genome and able to replicate efficiently when transfected into a susceptible cell line without reducing the growth rate of the cell line by more than 10 fold. The sequences are useful for screening for anti-HCV therapeutics, for detecting antibodies to HCV in a biological sample such as blood, serum, plasma, blood cells, lymphocytes, or liver cells from a subject, for deriving authentic HCV components such as replication-competent non-infectious, replication-defective infection-component, and replication-defective non-infectious HCV, in gene therapy or gene vaccination targeted to hepatic tissue for treating an animal infected or susceptible to HCV infection and for studying HCV infection and propagation. The present sequence is a clone of a fragment of the HCV genome designated HCV24

XX

SQ Sequence 7992 BP; 1648 A; 2369 C; 2242 G; 1733 T; 0 U; 0 Other;

XX

Query Match 99.9%; Score 7984; DB 6; Length 7992;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 7987; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY

1 GCCAGCCCCGATTGGGGGCGACACTCCACATAGATCACTCCCTGTGAGGAACACTG 60

Db

1 GCCAGCCCCGATTGGGGGCGACACTCCACATAGATCACTCCCTGTGAGGAACACTG 60

QY

61 TCTTCACGAGAAAGCGTCTAGCATGGGCTGTAGTGTAGTGTGTCGACCTCCAGGAC 120

Db

61 TCTTCACGAGAAAGCGTCTAGCATGGGCTGTAGTGTAGTGTGTCGACCTCCAGGAC 120

QY

121 CCCCCCTCCGGGAGAGCCATAGTGTCTGCGAACCGGTGAGTACACCGGAATGGCAG 180

Db

121 CCCCCCTCCGGGAGAGCCATAGTGTCTGCGAACCGGTGAGTACACCGGAATGGCAG 180

QY

181 GACGACCGGGTCTCTTTCTTGGATCAACCCGCTCAATGCTGAGATTGGCGTGCCTCC 240

Db

181 GACGACCGGGTCTCTTTCTTGGATCAACCCGCTCAATGCTGAGATTGGCGTGCCTCC 240

QY 241 GCGAGACTGCTAGCCGAGTAGTGTGGSTCGGAAAGCCCTTGTGTAATCTGCTGATAGG 300
 Db |||||
 241 GCGAGACTGCTAGCCGAGTAGTGTGGSTCGGAAAGCCCTTGTGTAATCTGCTGATAGG 300
 QY 301 GTGCTTGGAGTGCCTCCGGAGGTCTGTAGACCTGTGACCATGACGAAATCCTAAAC 360
 Db |||||
 301 GTGCTTGGAGTGCCTCCGGAGGTCTGTAGACCTGTGACCATGACGAAATCCTAAAC 360
 QY 361 CTCRAAGAAAACAAAGGCGCCATGATGAAACAGATGGAATGCAAGATCCTAAAC 420
 Db |||||
 361 CTCRAAGAAAACAAAGGCGCCATGATGAAACAGATGGAATGCAAGATCCTAAAC 420
 QY 421 CGGCGCTTGGGTGAGAGGCTATTGGCTATGACTGGGCAACAGACAAATCGCTGCT 480
 Db |||||
 421 CGGCGCTTGGGTGAGAGGCTATTGGCTATGACTGGGCAACAGACAAATCGCTGCT 480
 QY 481 CTGATGCGCGCTGCTCGGCTGTGAGCGAGGCGCCCGGTTCTTTTGTCAAGACCG 540
 Db |||||
 481 CTGATGCGCGCTGCTCGGCTGTGAGCGAGGCGCCCGGTTCTTTTGTCAAGACCG 540
 QY 541 ACCTGTCCGCTGCTGATGAATGAACTGAGGAGGAGGAGCGGCTATCGTGGCTGGCA 600
 Db |||||
 541 ACCTGTCCGCTGCTGATGAATGAACTGAGGAGGAGGAGCGGCTATCGTGGCTGGCA 600
 QY 601 CGAGCGGCTTCTTGGCGAGCTGTGCTCGACGTTGTCACTGAAGCGGAGGAGGACTGGC 660
 Db |||||
 601 CGAGCGGCTTCTTGGCGAGCTGTGCTCGACGTTGTCACTGAAGCGGAGGAGGACTGGC 660
 QY 661 TGTATTTGGGCGAGTCCGGGAGGATCTCTGTCACTCACTTGTCTCTGCGGAGA 720
 Db |||||
 661 TGTATTTGGGCGAGTCCGGGAGGATCTCTGTCACTCACTTGTCTCTGCGGAGA 720
 QY 721 AAGTATCCATCATGCTGCTGATGCAATGCGGCGGATCTCTGTCACTCACTTGTCTCTGCGGAGA 780
 Db |||||
 721 AAGTATCCATCATGCTGCTGATGCAATGCGGCGGATCTCTGTCACTCACTTGTCTCTGCGGAGA 780
 QY 781 CATTCGACCAACAAAGCGAAACATCGCATCGAGCGAGCATCGATCGATGGAAGCGGTC 840
 Db |||||
 781 CATTCGACCAACAAAGCGAAACATCGCATCGAGCGAGCATCGATCGATGGAAGCGGTC 840
 QY 841 TTGTCGATCAGATGATCTGAGCAAGAGATCAGGGGTTCGCCAGCGCACTGTTCG 900
 Db |||||
 841 TTGTCGATCAGATGATCTGAGCAAGAGATCAGGGGTTCGCCAGCGCACTGTTCG 900
 QY 901 CCAGGCTCAAGGCGGCATGCGCGAGGATCTCGTGTGACCCATGCGCATGCGATGCGT 960
 Db |||||
 901 CCAGGCTCAAGGCGGCATGCGCGAGGATCTCGTGTGACCCATGCGCATGCGATGCGT 960
 QY 961 GCTTGGCGAATATCATGTTGGAATAATGGCGCTTTTCTGGAATCATCGACTGTGGCGGCG 1020
 Db |||||
 961 GCTTGGCGAATATCATGTTGGAATAATGGCGCTTTTCTGGAATCATCGACTGTGGCGGCG 1020
 QY 1021 TGGGTGTGCGGACCGCTATCAGGACATAGCTTGGCTACCGTGATATGCTGAAGAGC 1080
 Db |||||
 1021 TGGGTGTGCGGACCGCTATCAGGACATAGCTTGGCTACCGTGATATGCTGAAGAGC 1080
 QY 1081 TTGCGGCGAATGAGGCTGACCGCTTCTGCTGCTTTAGGATACCGCTCCCGATTGCG 1140
 Db |||||
 1081 TTGCGGCGAATGAGGCTGACCGCTTCTGCTGCTTTAGGATACCGCTCCCGATTGCG 1140
 QY 1141 AGCGATCGCTTCTATCGCTTCTTACGAGTCTCTGAGTTTAAACAGACCAACAG 1200
 Db |||||
 1141 AGCGATCGCTTCTATCGCTTCTTACGAGTCTCTGAGTTTAAACAGACCAACAG 1200
 QY 1201 GTTTCCTCTAGCGGATCAATTCGCGCTCTCTCCCTCCCGCTTAAAGTACTGGC 1260
 Db |||||
 1201 GTTTCCTCTAGCGGATCAATTCGCGCTCTCTCCCTCCCGCTTAAAGTACTGGC 1260
 QY 1261 CGAAGCCGCTTGAATAAGGCGGCTGCTGCTTGTCTATATGTTTCCACCATATTG 1320
 Db |||||
 1261 CGAAGCCGCTTGAATAAGGCGGCTGCTGCTTGTCTATATGTTTCCACCATATTG 1320

QY 1321 CCGTCTTTTGGCAATGTGAGGCGCCGGAACCTTGCCCTGTCTTCTTGACGAGCATTCCT 1380
 Db |||||
 1321 CCGTCTTTTGGCAATGTGAGGCGCCGGAACCTTGCCCTGTCTTCTTGACGAGCATTCCT 1380
 QY 1381 AGGGTCTTTTCCCTCTCTCGCCAAAGGAATGCAAGGTCTGTTGAATGTCTGTAAGGAACA 1440
 Db |||||
 1381 AGGGTCTTTTCCCTCTCTCGCCAAAGGAATGCAAGGTCTGTTGAATGTCTGTAAGGAACA 1440
 QY 1441 GTTCTCTGGAAGCTTCTTGAAGACAAACACCTCTGAGGACCCCTTTGCGAGGAGCGG 1500
 Db |||||
 1441 GTTCTCTGGAAGCTTCTTGAAGACAAACACCTCTGAGGACCCCTTTGCGAGGAGCGG 1500
 QY 1501 AACCCGCCACCTGCGGACAGGTGCTCTGCGGCCAAAGCCACGCTGTATAGATACACT 1560
 Db |||||
 1501 AACCCGCCACCTGCGGACAGGTGCTCTGCGGCCAAAGCCACGCTGTATAGATACACT 1560
 QY 1561 GCAAGGCGGACAAACCCAGTGCACGTTGTGAGTTGGATGAGTTGGAAGAGTCAAA 1620
 Db |||||
 1561 GCAAGGCGGACAAACCCAGTGCACGTTGTGAGTTGGATGAGTTGGAAGAGTCAAA 1620
 QY 1621 TGGCTCTCTCAAGCGTATTCAACAGGCGTGAAGGATGCCAGAGGATACCCCATGT 1680
 Db |||||
 1621 TGGCTCTCTCAAGCGTATTCAACAGGCGTGAAGGATGCCAGAGGATACCCCATGT 1680
 QY 1681 ATGGGATCTGATCTGCGGCTCTGCGTGCACATGCTTTACATGTTTGTAGTTCGAGGTTAAAA 1740
 Db |||||
 1681 ATGGGATCTGATCTGCGGCTCTGCGTGCACATGCTTTACATGTTTGTAGTTCGAGGTTAAAA 1740
 QY 1741 AACGCTTAGGCGCCCGGAAACACAGGAGCGTGGTTTCTTTGAAAAACAGTAAATACC 1800
 Db |||||
 1741 AACGCTTAGGCGCCCGGAAACACAGGAGCGTGGTTTCTTTGAAAAACAGTAAATACC 1800
 QY 1801 ATGGCGCTATTACGCGCTACTCCCAACAGCGAGGCGCTACTTGGCTGCATCATCACT 1860
 Db |||||
 1801 ATGGCGCTATTACGCGCTACTCCCAACAGCGAGGCGCTACTTGGCTGCATCATCACT 1860
 QY 1861 AGCCTCACAGGCGGACAGGAAACAGGTCGAGGAGGAGTCCAGGTGTCTCCACCGCA 1920
 Db |||||
 1861 AGCCTCACAGGCGGACAGGAAACAGGTCGAGGAGGAGTCCAGGTGTCTCCACCGCA 1920
 QY 1921 ACACATCTTTCTGCGGCTGCGTCAATGCGGTGTGTTGGACTGTCTATCATGTGTC 1980
 Db |||||
 1921 ACACATCTTTCTGCGGCTGCGTCAATGCGGTGTGTTGGACTGTCTATCATGTGTC 1980
 QY 1981 GGTCAAAGACCTTTCGCGGCCCAAGGCGCCAAATCACCCAAATGTACACCAATGTGGAC 2040
 Db |||||
 1981 GGTCAAAGACCTTTCGCGGCCCAAGGCGCCAAATCACCCAAATGTACACCAATGTGGAC 2040
 QY 2041 CAGGACCTGCTGCGGTGGAAGCGCCCGGCGCGCTTCTTGACACCATGCACTGC 2100
 Db |||||
 2041 CAGGACCTGCTGCGGTGGAAGCGCCCGGCGCGCTTCTTGACACCATGCACTGC 2100
 QY 2101 GCGAGCTGCGACCTTTTACTTGTGTCAGGAGGATGCGATGTCAATCCGTTGCGCGGCGG 2160
 Db |||||
 2101 GCGAGCTGCGACCTTTTACTTGTGTCAGGAGGATGCGATGTCAATCCGTTGCGCGGCGG 2160
 QY 2161 GCGGACAGCGGAGGCTACTCTCCCGCGGCGCTCTCTACTTGAAGGCTCTTCG 2220
 Db |||||
 2161 GCGGACAGCGGAGGCTACTCTCCCGCGGCGCTCTCTACTTGAAGGCTCTTCG 2220
 QY 2221 GCGGTCACCTGCTCTGCGGTCGAGGCGCTGTGGGCACTTTTCGGGCTGCGGCTGTC 2280
 Db |||||
 2221 GCGGTCACCTGCTCTGCGGTCGAGGCGCTGTGGGCACTTTTCGGGCTGCGGCTGTC 2280
 QY 2281 ACCGAGGCTGCGAAGCGGCTGCACTTTGTATCCCGTGCAGTCTATCGAAACCACTATG 2340
 Db |||||
 2281 ACCGAGGCTGCGAAGCGGCTGCACTTTGTATCCCGTGCAGTCTATCGAAACCACTATG 2340
 QY 2341 CGGTCCCGGCTTTTCAAGGCAACTCTGTCCTCCCGCGGACCGGACGATTCAGGTG 2400
 Db |||||
 2341 CGGTCCCGGCTTTTCAAGGCAACTCTGTCCTCCCGCGGACCGGACGATTCAGGTG 2400
 QY 2401 GCCCATCTACGCGCCCTACTGTTAGCGCAAGAGCACTAAGGTGCGGCTGCGTATGCA 2460

3481	CTGCTAGCATACACAGCTACGGTGTGGCGCAGGGCTCAGGCTCCACCTCCATCGTGGAC	3540
3541	CAAAATGTGAAGTGTCTCATACGGCTAAAGCCTTACGCTGCAGCGGCCAACCGCCCTGTG	3600
3541	CAAAATGTGAAGTGTCTCATACGGCTTAAAGCCTTACGCTGCAGCGGCCAACCGCCCTGTG	3600
3601	TATAGGCTGGAGCCGTTCAAAAACGAGGTTACTACACACACCCCATTAACCAATACATC	3660
3601	TATAGGCTGGAGCCGTTCAAAAACGAGGTTACTACACACACCCCATTAACCAATACATC	3660
3661	ATGGCATGATGTGCGCTGACCTGGAGTGTGCTGACAGCACCTGGTGTCTGGTAGGGGA	3720
3661	ATGGCATGATGTGCGCTGACCTGGAGTGTGCTGACAGCACCTGGTGTCTGGTAGGGGA	3720
3721	GTCTTACAGCTCTGGCGCGTATTGCTGACAAACAGGAGCTGGTCAATGTGGGAGG	3780
3721	GTCTTACAGCTCTGGCGCGTATTGCTGACAAACAGGAGCTGGTCAATGTGGGAGG	3780
3781	ATCATCTTGTCCGAAAGCGCGCATCATTTCCGACAGGGAAGTCTTTTACCGGAGTTC	3840
3781	ATCATCTTGTCCGAAAGCGCGCATCATTTCCGACAGGGAAGTCTTTTACCGGAGTTC	3840
3841	GATGAGTGAAGAGTGGCGCTCACCTCTTACATCGAAGGGAATGAGCTCGCC	3900
3841	GATGAGTGAAGAGTGGCGCTCACCTCTTACATCGAAGGGAATGAGCTCGCC	3900
3901	GAAACAATTCAGAGAGGCAATCGGTTGTCGAAACAGCAACAGCAAGCGGAGCT	3960
3901	GAAACAATTCAGAGAGGCAATCGGTTGTCGAAACAGCAACAGCAAGCGGAGCT	3960
3961	GCTGCTCCGCTGGTGAATTCAGTGGCGGACCTCGAAGCTTCTGGCGGAGCATATG	4020
3961	GCTGCTCCGCTGGTGAATTCAGTGGCGGACCTCGAAGCTTCTGGCGGAGCATATG	4020
4021	TGGAATTTTCATCAGCGGATCAATATTTAGCAGGCTTGTCCACTCTGCTCGCAACCC	4080
4021	TGGAATTTTCATCAGCGGATCAATATTTAGCAGGCTTGTCCACTCTGCTCGCAACCC	4080
4081	GGATAGATCACTGATGGCATTCACGCTCTATCAACAGCGCGCTCAACCCACAT	4140
4081	GGATAGATCACTGATGGCATTCACGCTCTATCAACAGCGCGCTCAACCCACAT	4140
4141	ACCCTCTGTTTAAACATCTCGGGGATGGGTGGCGGCCAACTGCTCTCCACGGCT	4200
4141	ACCCTCTGTTTAAACATCTCGGGGATGGGTGGCGGCCAACTGCTCTCCACGGCT	4200
4201	GCTTCTGCTTCTGAGCGCCGCTGCTGAGCGGCTGTTGGCAGCATAGAGCTTGGG	4260
4201	GCTTCTGCTTCTGAGCGCCGCTGCTGAGCGGCTGTTGGCAGCATAGAGCTTGGG	4260
4261	AAGGTCTTGTGGATATTTTGGCAGGTTATGGAGCAGGGGTGGCAGCGGCTCGTGGCC	4320
4261	AAGGTCTTGTGGATATTTTGGCAGGTTATGGAGCAGGGGTGGCAGCGGCTCGTGGCC	4320
4321	TTTAAAGGTATGAGCGCGGATGCTTCCACCGAGGACCTGCTAACCTTCTCCCTGCT	4380
4321	TTTAAAGGTATGAGCGCGGATGCTTCCACCGAGGACCTGCTAACCTTCTCCCTGCT	4380
4381	ATCCTCTCCCTGCGCCCTAGTGTGCGGGTGTGCTGCGAGCGATPACTGCGTGGCAC	4440
4381	ATCCTCTCCCTGCGCCCTAGTGTGCGGGTGTGCTGCGAGCGATPACTGCGTGGCAC	4440
4441	GTGGGCGCCAGGGGAGGGGCTGTGCAAGTGAACCGGCTGTAGCGTTCGCTTCGGG	4500
4441	GTGGGCGCCAGGGGAGGGGCTGTGCAAGTGAACCGGCTGTAGCGTTCGCTTCGGG	4500
4501	GGTAAACACGCTTCCCGCCAGCACTATGCTGAGAGCGAGCTGAGCAGCGTGTCACT	4560
4501	GGTAAACACGCTTCCCGCCAGCACTATGCTGAGAGCGAGCTGAGCAGCGTGTCACT	4560
4561	CAGATCTCTCTAGTCTTACCATCAGCTCAGCTGTGAGAGGCTTCCAGTGTGATCAAC	4620
4561	CAGATCTCTCTAGTCTTACCATCAGCTCAGCTGTGAGAGGCTTCCAGTGTGATCAAC	4620

2401	GGCCATCTACACGCCCTACTGCTAGCGGAGAGCACTAAGGTGCGGCTGCGTATGCA	2460
2461	GGCCAGGGTATAGGTGCTTGTCTGAACCGCTCGTCCCGCCACCTTAGTGTTCGGG	2520
2461	GGCCAGGGTATAGGTGCTTGTCTGAACCGCTCGTCCCGCCACCTTAGTGTTCGGG	2520
2521	GGGTATATGCTAAGGCACATGTTATCGACCTTAACAATCAGAACCGGGGTAAAGCAATC	2580
2521	GGGTATATGCTAAGGCACATGTTATCGACCTTAACAATCAGAACCGGGGTAAAGCAATC	2580
2581	ACCAACGGGTGCGCCATCAAGTATCCACCTATGCAAGTTCCTGCGAGCGGTGCTG	2640
2581	ACCAACGGGTGCGCCATCAAGTATCCACCTATGCAAGTTCCTGCGAGCGGTGCTG	2640
2641	TCTGGGGCGGCTATGACATCATATATGATGAGTGCACCTCAACTGACCTGACCACT	2700
2641	TCTGGGGCGGCTATGACATCATATATGATGAGTGCACCTCAACTGACCTGACCACT	2700
2701	ATCCTGGGCATCGGCACAGTCTCTGGAACAGCGGAGCGGCTGGAGCGGACTGTCGTG	2760
2701	ATCCTGGGCATCGGCACAGTCTCTGGAACAGCGGAGCGGCTGGAGCGGACTGTCGTG	2760
2761	CTGCGCACCGCTACGCTTCGGGATCGGTCACCGTCCGACATCCAAACATCGAGAGGTG	2820
2761	CTGCGCACCGCTACGCTTCGGGATCGGTCACCGTCCGACATCCAAACATCGAGAGGTG	2820
2821	GCTCTGTCCAGCTCGGAGAAATCCCTTTTATGGCAAGGCACTCCCATCGAGACCATC	2880
2821	GCTCTGTCCAGCTCGGAGAAATCCCTTTTATGGCAAGGCACTCCCATCGAGACCATC	2880
2881	AAGGGGGGAGGACCTCATTTTCTGCCATTCGCAATTCGCAAGGAAATGATGAGCTCGCGG	2940
2881	AAGGGGGGAGGACCTCATTTTCTGCCATTCGCAATTCGCAAGGAAATGATGAGCTCGCGG	2940
2941	AAGTGTGCGGCTCGGACTCAATGCTGATGATATACCGGGGCTTATGCTATCGGTC	3000
2941	AAGTGTGCGGCTCGGACTCAATGCTGATGATATACCGGGGCTTATGCTATCGGTC	3000
3001	ATACCAACTTAGCGGAGAGCTCAATGCTGAGCAACGAGCGCTCTAATGACGGGCTTACC	3060
3001	ATACCAACTTAGCGGAGAGCTCAATGCTGAGCAACGAGCGCTCTAATGACGGGCTTACC	3060
3061	GGCGAATTCGACTCAGTGTGATGCAATGCAATACATGCTGATGCTGATGCTGATGCTG	3120
3061	GGCGAATTCGACTCAGTGTGATGCAATGCAATACATGCTGATGCTGATGCTGATGCTG	3120
3121	CTGGACCCGACCTTACCATTTGAGAGCAGCGCTGCAACAGCGGCTGTCACGCTCG	3180
3121	CTGGACCCGACCTTACCATTTGAGAGCAGCGCTGCAACAGCGGCTGTCACGCTCG	3180
3181	CAGCGCGGAGGAGGAGTGTGAGAGGAGGATGGGATTTACAGGTTTGTGATCCAGGA	3240
3181	CAGCGCGGAGGAGGAGTGTGAGAGGAGGATGGGATTTACAGGTTTGTGATCCAGGA	3240
3241	GAAACGCGCTCGGGCATGTTGCAATTCCTCGGTTCTGTCGAGTGTGCTATGACGGGCTG	3300
3241	GAAACGCGCTCGGGCATGTTGCAATTCCTCGGTTCTGTCGAGTGTGCTATGACGGGCTG	3300
3301	GCTTGTGATGAGTCAAGCGCGGAGCTCAGTGTAGGTTGCGGCTTACCTTAAACACA	3360
3301	GCTTGTGATGAGTCAAGCGCGGAGCTCAGTGTAGGTTGCGGCTTACCTTAAACACA	3360
3361	CCAGGTTGCGGCTGCGGAGGACATCTGGAGTTCCTGGAGAGCGTCTTTACAGGCTC	3420
3361	CCAGGTTGCGGCTGCGGAGGACATCTGGAGTTCCTGGAGAGCGTCTTTACAGGCTC	3420
3421	ACCCACATAGAGCGGCTTCTGCGAGTAAAGCAGGAGGAGCACTTCCCTTAC	3480
3421	ACCCACATAGAGCGGCTTCTGCGAGTAAAGCAGGAGGAGCACTTCCCTTAC	3480
3481	CTGGTATGATACAGGCTACGGTGTGCGGAGGCTCAGGCTCCACCTTCCATCGTGGAC	3540
3481	CTGGTATGATACAGGCTACGGTGTGCGGAGGCTCAGGCTCCACCTTCCATCGTGGAC	3540

QY	4621	GAGGACTGCTCCACGCCATGCTCCGGCTCGTGGCTAAAGAGATGTTTGGGATTCGATATGC	4680
Db	4621	GAGGACTGCTCCACGCCATGCTCCGGCTCGTGGCTAAAGAGATGTTTGGGATTCGATATGC	4680
QY	4681	ACGGTGTTGACTGATTTCAAGACCTGGCTCCAGTCCAAGTCTCTGCGCGGATTCGCCGGA	4740
Db	4681	ACGGTGTTGACTGATTTCAAGACCTGGCTCCAGTCCAAGTCTCTGCGCGGATTCGCCGGA	4740
QY	4741	GTCCCTCTTCTTCATGTCAACGTGGGTACAAGGAGTCTGCGGGGCGACGCGATCATG	4800
Db	4741	GTCCCTCTTCTTCATGTCAACGTGGGTACAAGGAGTCTGCGGGGCGACGCGATCATG	4800
QY	4801	CAAAACCACTGCCCATGTGGAGCAGAGATCACCGACATGTGAAAACCGTTCATATGAG	4860
Db	4801	CAAAACCACTGCCCATGTGGAGCAGAGATCACCGACATGTGAAAACCGTTCATATGAG	4860
QY	4861	ATCGTGGGGCCTAGGACCTGTAGTAAACGTGGCATGGAACATTCGCCATTAACGGGTAC	4920
Db	4861	ATCGTGGGGCCTAGGACCTGTAGTAAACGTGGCATGGAACATTCGCCATTAACGGGTAC	4920
QY	4921	ACCACGGGCCCTGTCACGCCCTCCCGGCGCCAAATTTATTCTAGGGCGCTGTGGCGGGT	4980
Db	4921	ACCACGGGCCCTGTCACGCCCTCCCGGCGCCAAATTTATTCTAGGGCGCTGTGGCGGGT	4980
QY	4981	GCTGCTGAGGAGTACGTGGAGTTTACGCGGTGGGGATTTCCACTACGTGACGGGCGATG	5040
Db	4981	GCTGCTGAGGAGTACGTGGAGTTTACGCGGTGGGGATTTCCACTACGTGACGGGCGATG	5040
QY	5041	ACCACATGACACGTAAAGTGCCTGTACAGTTCGGGCCCGGAATCTTTCACAGAAGTG	5100
Db	5041	ACCACATGACACGTAAAGTGCCTGTACAGTTCGGGCCCGGAATCTTTCACAGAAGTG	5100
QY	5101	GATGGGGTGGGTGTGACAGGTACGCTCCAGCTGCGAACCCTCTTACGGGAGAGGTC	5160
Db	5101	GATGGGGTGGGTGTGACAGGTACGCTCCAGCTGCGAACCCTCTTACGGGAGAGGTC	5160
QY	5161	ACATTCCTGGTCCGGGTCAATCAATACCTGTTGGGTCAAGCTCCCATGGAGCCGAA	5220
Db	5161	ACATTCCTGGTCCGGGTCAATCAATACCTGTTGGGTCAAGCTCCCATGGAGCCGAA	5220
QY	5221	CCGGAGTAGCAGTGCTCACTTCATGCTCACGACCCCTCCCAATACCGCGGAGACG	5280
Db	5221	CCGGAGTAGCAGTGCTCACTTCATGCTCACGACCCCTCCCAATACCGCGGAGACG	5280
QY	5281	GCTAAGCGTAGGTGGCCACGGGATCTCCCGCTCTTGGCGAGCTCATCAGCTATCCAG	5340
Db	5281	GCTAAGCGTAGGTGGCCACGGGATCTCCCGCTCTTGGCGAGCTCATCAGCTATCCAG	5340
QY	5341	CTGTCTGGCCTTCCTTGAAGGCAACATGACTACCCGTCAATGACTCCCCCGAGCTGAC	5400
Db	5341	CTGTCTGGCCTTCCTTGAAGGCAACATGACTACCCGTCAATGACTCCCCCGAGCTGAC	5400
QY	5401	CTCATCGAGGCCAACTCTCTGTGGCGGAGAGATGGCGGGAACATCACCCCGTGGAG	5460
Db	5401	CTCATCGAGGCCAACTCTCTGTGGCGGAGAGATGGCGGGAACATCACCCCGTGGAG	5460
QY	5461	TCAGAAAAATAGGTAGTAAATTTTGGACTCTTTCAGCCGCTCCAAAGCGGAGGATGAG	5520
Db	5461	TCAGAAAAATAGGTAGTAAATTTTGGACTCTTTCAGCCGCTCCAAAGCGGAGGATGAG	5520
QY	5521	AGGGAAGTATCCGTTCCGGCGGAGATCTTCGGAGGTCCAGGAATTCCTCCAGCGATG	5580
Db	5521	AGGGAAGTATCCGTTCCGGCGGAGATCTTCGGAGGTCCAGGAATTCCTCCAGCGATG	5580
QY	5581	CCCATATGGGACGCCCCGATTTACAACTTCACTGTTAGTCTCTGGAAGACCCGGAC	5640
Db	5581	CCCATATGGGACGCCCCGATTTACAACTTCACTGTTAGTCTCTGGAAGACCCGGAC	5640
QY	5641	TACGTCCTCTCAGTGGTACACGGGTGTCAATTCGCGCTGCCAAGGCCCTCGATACCA	5700
Db	5641	TACGTCCTCTCAGTGGTACACGGGTGTCAATTCGCGCTGCCAAGGCCCTCGATACCA	5700

QY	5701	CTTCCACGGAGGAGGACGGTGTCTCTGTAGAAATCTACCGGTGCTTCTGCTTGGCG	5760
Db	5701	CCTCCACGGAGGAGGAGGACGGTGTCTCTGTAGAAATCTACCGGTGCTTCTGCTTGGCG	5760
QY	5761	GAGCTCGCCACAAAGACCTTTGGCGAGCTCGGAATCTCGGCCGTGACAGCGGCACGGCA	5820
Db	5761	GAGCTCGCCACAAAGACCTTTGGCGAGCTCGGAATCTCGGCCGTGACAGCGGCACGGCA	5820
QY	5821	ACGGGCTCTCTCTGACACAGCCCTCCGACGAGCGGAGCGGGATCTCGAGCTGAGTACGTAC	5880
Db	5821	ACGGGCTCTCTCTGACACAGCCCTCCGACGAGCGGAGCGGGATCTCGAGCTGAGTACGTAC	5880
QY	5881	TCCTTCATGCCCCCTTTGAGGGGAGCGGGGGATCCCGATCTCAGCGACGGGTCTTGG	5940
Db	5881	TCCTTCATGCCCCCTTTGAGGGGAGCGGGGGATCCCGATCTCAGCGACGGGTCTTGG	5940
QY	5941	TCTACCGTAAAGCGAGGAGCTAGTGAGGACGTGCTGTGCTGCTGATGTCCTACACATGG	6000
Db	5941	TCTACCGTAAAGCGAGGAGCTAGTGAGGACGTGCTGTGCTGCTGATGTCCTACACATGG	6000
QY	6001	ACAGCGGCCCTGATCACGCCATGCGTCGGGAGGAACCAAGCTGCCATCAATGACTGTG	6060
Db	6001	ACAGCGGCCCTGATCACGCCATGCGTCGGGAGGAACCAAGCTGCCATCAATGACTGTG	6060
QY	6061	AGCAACTCTTTGCTCCGTCACCAACCTTGCTATGCTACAACATCTCGACGCGCAAGC	6120
Db	6061	AGCAACTCTTTGCTCCGTCACCAACCTTGCTATGCTACAACATCTCGACGCGCAAGC	6120
QY	6121	CTGCGGACAGGAGAGGTACCTTTGACAGACTGAGGTCCTGAGCGACCACTACCGGAC	6180
Db	6121	CTGCGGACAGGAGAGGTACCTTTGACAGACTGAGGTCCTGAGCGACCACTACCGGAC	6180
QY	6181	GTGCTCAAGGAGATGAAGCGGAGCGGCTCCACAGTTAAGGCTAACTTCTATCCGTGAG	6240
Db	6181	GTGCTCAAGGAGATGAAGCGGAGCGGCTCCACAGTTAAGGCTAACTTCTATCCGTGAG	6240
QY	6241	GAAGCCTGTAAGCTGACGCGCCCCACATTCGCGCCAGATCTAAATTTGGCTATGGGCAAG	6300
Db	6241	GAAGCCTGTAAGCTGACGCGCCCCACATTCGCGCCAGATCTAAATTTGGCTATGGGCAAG	6300
QY	6301	GAGCTCCGGAACCTATCCAGCAGGCGGTTAACACATCCGCTCCGTGTGGAAGCACTTG	6360
Db	6301	GAGCTCCGGAACCTATCCAGCAGGCGGTTAACACATCCGCTCCGTGTGGAAGCACTTG	6360
QY	6361	CTGGAAGACACTGAGACACCAATTGACACCACCATCATGCGCAAAAATGAGTTTCTGC	6420
Db	6361	CTGGAAGACACTGAGACACCAATTGACACCACCATCATGCGCAAAAATGAGTTTCTGC	6420
QY	6421	GTCCACACGAGAGGGGGCCGACAGCTCGCCTTATCGTATTTCCAGATTTGGGG	6480
Db	6421	GTCCACACGAGAGGGGGCCGACAGCTCGCCTTATCGTATTTCCAGATTTGGGG	6480
QY	6481	GTTCTGTGTGCGAGAAATGGCCCTTACGATGTGCTTCCACCTCCCTCAGGCGGTG	6540
Db	6481	GTTCTGTGTGCGAGAAATGGCCCTTACGATGTGCTTCCACCTCCCTCAGGCGGTG	6540
QY	6541	ATGGGCTTTTCATCGGATTCGAATCTCTCTGGACAGCGGTGAGTTTCCTGFTGAAT	6600
Db	6541	ATGGGCTTTTCATCGGATTCGAATCTCTCTGGACAGCGGTGAGTTTCCTGFTGAAT	6600
QY	6601	GCTCGGAAGCGAAGAAATGCCCTATGGCTTCGCATATGACACCCGCTGTTTGACTCA	6660
Db	6601	GCTCGGAAGCGAAGAAATGCCCTATGGCTTCGCATATGACACCCGCTGTTTGACTCA	6660
QY	6661	ACGGTCACTGAGATGACATCCGCTGTGAGGAGTCAATCTACCAATGTTGACTTGGCC	6720
Db	6661	ACGGTCACTGAGATGACATCCGCTGTGAGGAGTCAATCTACCAATGTTGACTTGGCC	6720
QY	6721	CCGGAAGCCAGACGGCCATAGGTGCTCAGAGCGGCTTTACATCGGGGGCCCCCTG	6780
Db	6721	CCGGAAGCCAGACGGCCATAGGTGCTCAGAGCGGCTTTACATCGGGGGCCCCCTG	6780
QY	6781	ACTAATTTCTAAGCGCAACTCGGCTATCGCGGTGCGCGAGGGGTGTACTGACG	6840

[illegible]

xx

The invention relates to nucleic acid molecules comprising altered HCV NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV) internal ribosome entry site (IRES) region coding for one or more NS3, NS5A, or EMCV IRES mutations, respectively. The location of the mutations are detailed in the specification. Also included are (1) an expression vector comprising a nucleotide sequence coding for the altered nucleic acids, which is transcriptionally coupled to an exogenous promoter; (2) a recombinant cell human hepatoma cell comprising the altered nucleic acids; (3) a recombinant cell produced by introducing into a human hepatoma cell the altered nucleic acids; (4) producing an HCV (hepatitis C virus) replicon enhanced cell or which containing a functional HCV replicon; (5) an HCV replicon enhanced cells made in the method; and (6) measuring the ability of a compound to affect HCV activity. The HCV replicons and HCV replicon enhanced cells are useful in studying HCV replication and HCV expression, and HCV and host cell interactions, producing HCV RNA and proteins, and providing a system for measuring the ability of a compound to modulate one or more HCV activities e.g. to discover drugs which may treat HCV mediated diseases such as liver failure, cirrhosis and hepatocellular carcinoma. The present sequence is an HCV based vector pHCVneo.17 mutant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer using the HCV vector sequence appearing as ABK91412 and the information in Claim 16

xx SQ Sequence 10690 BP; 2335 A; 3045 C; 2907 G; 2403 T; 0 U; 0 Other;

Query Match 99.9%; Score 7984; DB 6; Length 10690;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 7987; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY	1	GCCAGCCCCGATTGGGGGCGACACTCCACCATAGATCACTCCCTGTGAGAACTACTG	60
Db	1	GCCAGCCCCGATTGGGGGCGACACTCCACCATAGATCACTCCCTGTGAGAACTACTG	60
QY	61	TCCTACGACAGAAAGCGTCTAGCCATCGGCTAGTATGAGTGTCTGCGAGCTCCAG	120
Db	61	TCCTACGACAGAAAGCGTCTAGCCATCGGCTAGTATGAGTGTCTGCGAGCTCCAG	120
QY	121	CCCCCTCCCGGAGAGCCATAGTGTCTGCGAAACCGGTGAGTACACCGAATGCGAG	180
Db	121	CCCCCTCCCGGAGAGCCATAGTGTCTGCGAAACCGGTGAGTACACCGAATGCGAG	180
QY	181	GACGACGGGTCTCTTCTTGATCAACCCGCTCAATGCTGAGATTTGGGCGTGCCCC	240
Db	181	GACGACGGGTCTCTTCTTGATCAACCCGCTCAATGCTGAGATTTGGGCGTGCCCC	240
QY	241	GCGAGACTGCTAGCCGAGTAGTCTGCGTCCGAAAGCCCTGTGTGTAATGCTGATAGG	300
Db	241	GCGAGACTGCTAGCCGAGTAGTCTGCGTCCGAAAGCCCTGTGTGTAATGCTGATAGG	300
QY	301	GTGCTTGGAGTSCCCCGGAGTCTCTGAGACCGTGACCATGACGACGAATCCTAAAC	360
Db	301	GTGCTTGGAGTSCCCCGGAGTCTCTGAGACCGTGACCATGACGACGAATCCTAAAC	360
QY	361	CTCAAGAAACCAAGGCGCGCCATGATTGAAACAGATGATTCGACGAGTTCTC	420
Db	361	CTCAAGAAACCAAGGCGCGCCATGATTGAAACAGATGATTCGACGAGTTCTC	420
QY	421	CGGCGCTTGGGTGGAGAGGCTATTTCGGCTATGACTGGGCAACAGACATCGGCTGCT	480
Db	421	CGGCGCTTGGGTGGAGAGGCTATTTCGGCTATGACTGGGCAACAGACATCGGCTGCT	480
QY	481	CTGATGCGCCGTGTTTCCGGCTGTGAGCGGCGCGGCTCTTTTGTTCAGACCG	540
Db	481	CTGATGCGCCGTGTTTCCGGCTGTGAGCGGCGCGGCTCTTTTGTTCAGACCG	540
QY	541	ACCTGTCGGTCCCTGAAATGAACTGACGACGAGCGCGGCTATCGTGGCTGGCA	600
Db	541	ACCTGTCGGTCCCTGAAATGAACTGACGACGAGCGCGGCTATCGTGGCTGGCA	600
QY	601	CGACGGGCGTCTCTTGGCGAGCTGTCTGAGCTGTCTACTGAAAGGGAAGGACTGGC	660
Db	601	CGACGGGCGTCTCTTGGCGAGCTGTCTGAGCTGTCTACTGAAAGGGAAGGACTGGC	660

QY	661	TGCTATTGGGCGAAGTGGCGGGCAGGAGTCTCTGTCTATCTACCTTGTCTCTGCGGAGA	720
Db	661	TGCTATTGGGCGAAGTGGCGGGCAGGAGTCTCTGTCTATCTACCTTGTCTCTGCGGAGA	720
QY	721	AAGTATCCATCATGCTGATGCAATGCGGCGGCTGCATACGCTTGCATCCGGTACTGCG	780
Db	721	AAGTATCCATCATGCTGATGCAATGCGGCGGCTGCATACGCTTGCATCCGGTACTGCG	780
QY	781	CATTCCGACCAACCAAGCGGAAACATCCCATCGAGCGAGCAGTACTCGATGAGGCGGTG	840
Db	781	CATTCCGACCAACCAAGCGGAAACATCCCATCGAGCGAGCAGTACTCGATGAGGCGGTG	840
QY	841	TTGTCGATCAGATGATCTGACGAGAGCATCAGGGCTCGCGCCAGCCGAACTGTTTCG	900
Db	841	TTGTCGATCAGATGATCTGACGAGAGCATCAGGGCTCGCGCCAGCCGAACTGTTTCG	900
QY	901	CCAGGCTCAAGCGCGCATGCCGAGCGGAGGATCTCTGTCGATGCCATGCGCGATGCT	960
Db	901	CCAGGCTCAAGCGCGCATGCCGAGCGGAGGATCTCTGTCGTCGATGCCATGCGCGATGCT	960
QY	961	GCTTCCCGAATATCATGCTGGAATATGCGCGCTTTCTGGAATTCATCGACTGCGCGGC	1020
Db	961	GCTTCCCGAATATCATGCTGGAATATGCGCGCTTTCTGGAATTCATCGACTGCGCGGC	1020
QY	1021	TGGGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGCTGATTTCTGCAAGAGC	1080
Db	1021	TGGGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGCTGATTTCTGCAAGAGC	1080
QY	1081	TTGCGCGGATGCGGCTGACCGCTTCTCTGCTTTACGATATCGCGCTCCCGATTTCG	1140
Db	1081	TTGCGCGGATGCGGCTGACCGCTTCTCTGCTTTACGATATCGCGCTCCCGATTTCG	1140
QY	1141	AGGCGATCGCTTCTATCGCTTCTTACGAGTCTCTGAGTTTAAACAGACACAAAGC	1200
Db	1141	AGGCGATCGCTTCTATCGCTTCTTACGAGTCTCTGAGTTTAAACAGACACAAAGC	1200
QY	1201	GTTCCTCTAGCGGATCAATTCGCGCTCTCCCTCCCCCCCCCTAACGTTACTGGC	1260
Db	1201	GTTCCTCTAGCGGATCAATTCGCGCTCTCCCTCCCCCCCCCTAACGTTACTGGC	1260
QY	1261	CGAAGCGCTTGAATTAAGSCCGGTGCTTGTCTATATGTTATTTCCACCATATTG	1320
Db	1261	CGAAGCGCTTGAATTAAGSCCGGTGCTTGTCTATATGTTATTTCCACCATATTG	1320
QY	1321	CCGCTCTTTTGGCAATGTGAGGCGCGGAAACCTGCGCTCTCTTCTGACGAGATTCCT	1380
Db	1321	CCGCTCTTTTGGCAATGTGAGGCGCGGAAACCTGCGCTCTCTTCTGACGAGATTCCT	1380
QY	1381	AGGGGTCTTTCCTCTCGCCAAAGGAATGCAAGGTCTCTGTAATCTGTAAGGAGCA	1440
Db	1381	AGGGGTCTTTCCTCTCGCCAAAGGAATGCAAGGTCTCTGTAATCTGTAAGGAGCA	1440
QY	1441	GTTCCTCTGAGAGCTTCTTGAAGACAAACAGCTGTGTAGCGACCTTTGCGAGCGCG	1500
Db	1441	GTTCCTCTGAGAGCTTCTTGAAGACAAACAGCTGTGTAGCGACCTTTGCGAGCGCG	1500
QY	1501	AAACCCCCACCTTGGCGACAGGTGCTCTGCGGCCAAAGCCAGCTGTATAGATACACT	1560
Db	1501	AAACCCCCACCTTGGCGACAGGTGCTCTGCGGCCAAAGCCAGCTGTATAGATACACT	1560
QY	1561	GCAAGGCGGCAACACCCAGTGCACCGTGTGAGTGTGATAGTTGTGGAAGAGTCAAA	1620
Db	1561	GCAAGGCGGCAACACCCAGTGCACCGTGTGAGTGTGATAGTTGTGGAAGAGTCAAA	1620
QY	1621	TGGCTCTCTCAAGCGTATTCAAGGGGCTGAAGGATGCCAGAGGTACCCATTGT	1680
Db	1621	TGGCTCTCTCAAGCGTATTCAAGGGGCTGAAGGATGCCAGAGGTACCCATTGT	1680
QY	1681	ATGGGATCTGATCTGGGCGCTCGGTGACATGCTTTTACATGTTTGTGAGGTTAAA	1740
Db	1681	ATGGGATCTGATCTGGGCGCTCGGTGACATGCTTTTACATGTTTGTGAGGTTAAA	1740

Qy	1741	AACGCTCTAGCGCCCGGAAACCAAGGAGCGTGGTTTCCTTTGAAACACGATAATACC	1800
Db	1741	AACGCTCTAGCGCCCGGAAACCAAGGAGCGTGGTTTCCTTTGAAACACGATAATACC	1800
Qy	1801	ATGGCGCTTATTAGCGCTTACTCCCAACAGACGCGAGCGCTTACTTGGCTGCATCATCACT	1860
Db	1801	ATGGCGCTTATTAGCGCTTACTCCCAACAGACGCGAGCGCTTACTTGGCTGCATCATCACT	1860
Qy	1861	AGCCTCAAGCGCGGAGCAGGAACAGGTCCAGGGGAGGTCCAGGTGGTCTCCACCGCA	1920
Db	1861	AGCCTCAAGCGCGGAGCAGGAACAGGTCCAGGGGAGGTCCAGGTGGTCTCCACCGCA	1920
Qy	1921	ACACAAATCTTTCCTGGGACCTCGGTCAATGGCGTGGTGGAGCTGTCTATCATGGTGGC	1980
Db	1921	ACACAAATCTTTCCTGGGACCTCGGTCAATGGCGTGGTGGAGCTGTCTATCATGGTGGC	1980
Qy	1981	GGCTCAAGAGCCCTTGGCGGCCCAAGGGCCCAATCACCAAAATGTACCAAAATGTGGAC	2040
Db	1981	GGCTCAAGAGCCCTTGGCGGCCCAAGGGCCCAATCACCAAAATGTACCAAAATGTGGAC	2040
Qy	2041	CAGGACCTCGTGGCTGGCAAGCGCCCGCGGGCGGTTCCTTGACACCATGCACTGCG	2100
Db	2041	CAGGACCTCGTGGCTGGCAAGCGCCCGCGGGCGGTTCCTTGACACCATGCACTGCG	2100
Qy	2101	GGCAGCTCGGACCTTTTACTTGGTCAAGAGGATGCCGATGTCATTCGGTGGCGCGGG	2160
Db	2101	GGCAGCTCGGACCTTTTACTTGGTCAAGAGGATGCCGATGTCATTCGGTGGCGCGGG	2160
Qy	2161	GGCGACAGCGGGGAGGCTACTCTCCCGCGCGCGCTCTCTTGAAGGGCTCTTCG	2220
Db	2161	GGCGACAGCGGGGAGGCTACTCTCCCGCGCGCGCTCTCTTGAAGGGCTCTTCG	2220
Qy	2221	GGCGGTCCACTGCTCTGCGCCCTCGGGGACCGTGTGGGCATCTTTCGGGCTCGCGTGGC	2280
Db	2221	GGCGGTCCACTGCTCTGCGCCCTCGGGGACCGTGTGGGCATCTTTCGGGCTCGCGTGGC	2280
Qy	2281	ACCCGAGGGGTTGCGAAGCGGTGGACTTTGTACCGGTGAGTCTATGGAACCACTATG	2340
Db	2281	ACCCGAGGGGTTGCGAAGCGGTGGACTTTGTACCGGTGAGTCTATGGAACCACTATG	2340
Qy	2341	CGGTCCCGGTCTTACAGGACAACTCGTCCCTCGCGCGTACCGCAGACATTCACAGTG	2400
Db	2341	CGGTCCCGGTCTTACAGGACAACTCGTCCCTCGCGCGTACCGCAGACATTCACAGTG	2400
Qy	2401	GCCCATCTACAGCCCTTACTGGTAGCGGCAAGACACTAAGGTGGCGGTGGTATGCA	2460
Db	2401	GCCCATCTACAGCCCTTACTGGTAGCGGCAAGACACTAAGGTGGCGGTGGTATGCA	2460
Qy	2461	GCCAAAGGTTAAGGTGCTTGTCTGAACCCGTGGTGGCGGCGGCTAGGTTTCGGG	2520
Db	2461	GCCAAAGGTTAAGGTGCTTGTCTGAACCCGTGGTGGCGGCGGCTAGGTTTCGGG	2520
Qy	2521	GGGTATATCTAAGGCACATGTATCGACCCCTAAACATCAGAACCGGGGTAAGGACCATC	2580
Db	2521	GGGTATATCTAAGGCACATGTATCGACCCCTAAACATCAGAACCGGGGTAAGGACCATC	2580
Qy	2581	ACCAAGGTTGCCCGCATCAGCTACTCCACTATGGGAAAGTTTCTTGGCGGCGGTGGTGC	2640
Db	2581	ACCAAGGTTGCCCGCATCAGCTACTCCACTATGGGAAAGTTTCTTGGCGGCGGTGGTGC	2640
Qy	2641	TCCTGGGCGGCTTATGACATCAATAATGTATGATGAGTGCCACTCAACTGACTCGACCACT	2700
Db	2641	TCCTGGGCGGCTTATGACATCAATAATGTATGATGAGTGCCACTCAACTGACTCGACCACT	2700
Qy	2701	ATCTGGGCGCATCGGACAGCTCTGGACCAAGCGGAGACGGGTGGAGCGCGACTCGTGGT	2760
Db	2701	ATCTGGGCGCATCGGACAGCTCTGGACCAAGCGGAGACGGGTGGAGCGCGACTCGTGGT	2760
Qy	2761	CTCGCCACCGGTACGCTTCGGGATCGGTACCGTGGCAGATCCCAACATCGAGGAGTG	2820
Db	2761	CTCGCCACCGGTACGCTTCGGGATCGGTACCGTGGCAGATCCCAACATCGAGGAGTG	2820
Qy	2821	GCTCTGTCCAGCACTGGAGAAATCCCTTTTATGGCAAGGCAATCCCTCATCGAGACCATC	2880
Db	2821	GCTCTGTCCAGCACTGGAGAAATCCCTTTTATGGCAAGGCAATCCCTCATCGAGACCATC	2880
Qy	2881	AAGGGGGAGGACACCTCTATTTCTGCAATCCAAAGAAATGTGTATGAGCTCGCGCG	2940
Db	2881	AAGGGGGAGGACACCTCTATTTCTGCAATCCAAAGAAATGTGTATGAGCTCGCGCG	2940
Qy	2941	AAGCTGTCCCGCTCGGACTCAATGTGTAGTATATTTACCGGGGCTTGTATTCGGTC	3000
Db	2941	AAGCTGTCCCGCTCGGACTCAATGTGTAGTATATTTACCGGGGCTTGTATTCGGTC	3000
Qy	3001	ATACCAACTAGCGAGACGCTCAATGTGTAGTATATTTACCGGGGCTTGTATTCGGTC	3060
Db	3001	ATACCAACTAGCGAGACGCTCAATGTGTAGTATATTTACCGGGGCTTGTATTCGGTC	3060
Qy	3061	GGCGATTTTCGACTCAGTGATCGACTGCAATATGTGTACCCAGACAGTCTGACTTACG	3120
Db	3061	GGCGATTTTCGACTCAGTGATCGACTGCAATATGTGTACCCAGACAGTCTGACTTACG	3120
Qy	3121	CTGGACCCGACCTTTCACCATTTGAGACGACCGGTGCCAAGCGCGGTGTGACTGCG	3180
Db	3121	CTGGACCCGACCTTTCACCATTTGAGACGACCGGTGCCAAGCGCGGTGTGACTGCG	3180
Qy	3181	CAGCGGCGAGGAGGACGCTGTGTAGGGGAGGATGGGCAATTTACAGGTTTGTGACTCCAG	3240
Db	3181	CAGCGGCGAGGAGGACGCTGTGTAGGGGAGGATGGGCAATTTACAGGTTTGTGACTCCAG	3240
Qy	3241	GAAAGGCGCTCGGGCATGTTCCGTTCTCGGTTCCTGTCGAGTGTATGACGCGGGCTGT	3300
Db	3241	GAAAGGCGCTCGGGCATGTTCCGTTCTCGGTTCCTGTCGAGTGTATGACGCGGGCTGT	3300
Qy	3301	GCTTGTGTACGAGCTCACGCGCGCGGACCTCAGTTAGTTTGGGGCTTACCTTAACACA	3360
Db	3301	GCTTGTGTACGAGCTCACGCGCGCGGACCTCAGTTAGTTTGGGGCTTACCTTAACACA	3360
Qy	3361	CCAGGGTTGCCGCTGTGCCAGGACCATCTGGAGTTCTGGGAGGCGTCTTTACAGGCTTC	3420
Db	3361	CCAGGGTTGCCGCTGTGCCAGGACCATCTGGAGTTCTGGGAGGCGTCTTTACAGGCTTC	3420
Qy	3421	ACCCACATAGAGCCCATTTCTTGTCCAGACTTAAGCAGGAGGAGCAACTTCCCTTAC	3480
Db	3421	ACCCACATAGAGCCCATTTCTTGTCCAGACTTAAGCAGGAGGAGCAACTTCCCTTAC	3480
Qy	3481	CTGGTAGCATACAGGCTACGGTGTGCGGCGGCTCAGGCTCAGCTCCATCGTGGGAC	3540
Db	3481	CTGGTAGCATACAGGCTACGGTGTGCGGCGGCTCAGGCTCAGCTCCATCGTGGGAC	3540
Qy	3541	CAAAATGTGAAGTGTCTCATACGGCTAAAGCCTTACGCTGACGCGGCAAGCGCCCTGCTG	3600
Db	3541	CAAAATGTGAAGTGTCTCATACGGCTAAAGCCTTACGCTGACGCGGCAAGCGCCCTGCTG	3600
Qy	3601	TATAGGCTGGAGCGGCTTCAAAACAGAGTTTACTTACCAACACACCCCAATCAATCAATC	3660
Db	3601	TATAGGCTGGAGCGGCTTCAAAACAGAGTTTACTTACCAACACACCCCAATCAATCAATC	3660
Qy	3661	ATGGCATGATGTCGGCTGACCTGGAGGTGCTGACGAGGACCTGGGTGCTGGTAGGGGA	3720
Db	3661	ATGGCATGATGTCGGCTGACCTGGAGGTGCTGACGAGGACCTGGGTGCTGGTAGGGGA	3720
Qy	3721	GTCTTAGCAGCTGTGGCGGCTATTCCTGACAAACAGGAGCGGTGCTTGTGGGCGG	3780
Db	3721	GTCTTAGCAGCTGTGGCGGCTATTCCTGACAAACAGGAGCGGTGCTTGTGGGCGG	3780
Qy	3781	ATCATCTTGTCCGGAAGCGCGGCTCATTTCCGACAGGGAAGTCTTTTACCGGGAGTTC	3840
Db	3781	ATCATCTTGTCCGGAAGCGCGGCTCATTTCCGACAGGGAAGTCTTTTACCGGGAGTTC	3840
Qy	3841	GATGAGATGGAAGTGGCGCTCACCTCTTACATCGAAGGGAAGTACGCTCGCC	3900
Db	3841	GATGAGATGGAAGTGGCGCTCACCTCTTACATCGAAGGGAAGTACGCTCGCC	3900
Qy	3901	GAAACATTTCAACAGAGGCAATCGGGTGTGCTGCAAAACAGCCACCAAGCAGCGAGGCT	3960
Db	3901	GAAACATTTCAACAGAGGCAATCGGGTGTGCTGCAAAACAGCCACCAAGCAGCGAGGCT	3960

Db	3901	GAACAAATTC	AAAGAGGCAATCGGGTGTGTC	AAACAGCCACCAAGCAAGCGGAGGCT	3960
QY	3961	GCTGCTCCG	TGGTGGAAATCAAGTGGCGGAC	CCCTCGAAGCCCTTCTGGCGAAGCATATG	4020
Db	3961	GCTGCTCCG	TGGTGGAAATCAAGTGGCGGAC	CCCTCGAAGCCCTTCTGGCGAAGCATATG	4020
QY	4021	TGGAAATTC	CATCAGCGGGATACAATATATTTAG	CAGGCTTGTCCACTCTGCTTGGCAACCC	4080
Db	4021	TGGAAATTC	CATCAGCGGGATACAATATATTTAG	CAGGCTTGTCCACTCTGCTTGGCAACCC	4080
QY	4081	GGATATAGAT	CACTGATGCAATTCAGAGCTTATCA	CAGCCCGCTCAACACCCAAAT	4140
Db	4081	GGATATAGAT	CACTGATGCAATTCAGAGCTTATCA	CAGCCCGCTCAACACCCAAAT	4140
QY	4141	ACCTCTCCT	GTGTTTAAACATCTCGGGGGATGG	TGGCGCGCCCAACTTGTCTCCAGCGCT	4200
Db	4141	ACCTCTCCT	GTGTTTAAACATCTCGGGGGATGG	TGGCGCGCCCAACTTGTCTCCAGCGCT	4200
QY	4201	GCTTCTGCT	TTTGTAGGCGCGGATATGCTGAG	CGGCTGTGGCAGATAGGCTTTGGG	4260
Db	4201	GCTTCTGCT	TTTGTAGGCGCGGATATGCTGAG	CGGCTGTGGCAGATAGGCTTTGGG	4260
QY	4261	AAGGTGCTT	GTGGATATTTTTCGACAGTTATG	GACAGGGGTGGAGCGCGCTGTGGC	4320
Db	4261	AAGGTGCTT	GTGGATATTTTTCGACAGTTATG	GACAGGGGTGGAGCGCGCTGTGGC	4320
QY	4321	TTTAAAGT	CATGAGCGGCGAGATGCCCTCC	ACCGAGGACCTGGCTTAACCTACTCCCTGCT	4380
Db	4321	TTTAAAGT	CATGAGCGGCGAGATGCCCTCC	ACCGAGGACCTGGCTTAACCTACTCCCTGCT	4380
QY	4381	ATCCTCTCC	CTGCGGCTTAGTCTGCGGGTCTG	TGCGAGGATACCTGCTGCGCAC	4440
Db	4381	ATCCTCTCC	CTGCGGCTTAGTCTGCGGGTCTG	TGCGAGGATACCTGCTGCGCAC	4440
QY	4441	GTGGCCCA	GAGGGAGGGGCTGCTGAGTGA	TGAACTGAGGCTTACCAAGGCTTCA	4500
Db	4441	GTGGCCCA	GAGGGAGGGGCTGCTGAGTGA	TGAACTGAGGCTTACCAAGGCTTCA	4500
QY	4501	GGTAACCA	CGCTCTCCCCCAGCAGCACTAT	GTGCTGAGAGCGACGCTGAGCAGCTG	4560
Db	4501	GGTAACCA	CGCTCTCCCCCAGCAGCACTAT	GTGCTGAGAGCGACGCTGAGCAGCTG	4560
QY	4561	CAGATCTCT	CTAGTCTTACCATCACTCAGT	CTGCTGAGAGCGACGCTGAGCAGCTG	4620
Db	4561	CAGATCTCT	CTAGTCTTACCATCACTCAGT	CTGCTGAGAGCGACGCTGAGCAGCTG	4620
QY	4621	GAGGACTGT	CTCCAGCCATCTCGGCTCGTGG	TGAGATGTTGGATTTGGAATATGC	4680
Db	4621	GAGGACTGT	CTCCAGCCATCTCGGCTCGTGG	TGAGATGTTGGATTTGGAATATGC	4680
QY	4681	ACGGTGTGA	CTGATTTCAAGACCTGGCTCC	AGTCCAAAGCTCTGCGCGGATTTGG	4740
Db	4681	ACGGTGTGA	CTGATTTCAAGACCTGGCTCC	AGTCCAAAGCTCTGCGCGGATTTGG	4740
QY	4741	GTCCCTCTT	CTCATGTCAACGTGGGTACA	GGGAGTCTGGCGGGCGGACGCATCATG	4800
Db	4741	GTCCCTCTT	CTCATGTCAACGTGGGTACA	GGGAGTCTGGCGGGCGGACGCATCATG	4800
QY	4801	CAAAACCA	CTGCTTGGAGCACAGATCAC	CGGACATGTGAAAAAGGTTCCATGAGG	4860
Db	4801	CAAAACCA	CTGCTTGGAGCACAGATCAC	CGGACATGTGAAAAAGGTTCCATGAGG	4860
QY	4861	ATCGTGGG	CCCTAGGACCTGTAGTAA	CAGTGGCATGGAACATTTCCCATTAAC	4920
Db	4861	ATCGTGGG	CCCTAGGACCTGTAGTAA	CAGTGGCATGGAACATTTCCCATTAAC	4920
QY	4921	ACCAAGGG	CCCTGACGCGCTCCCGGCG	CCAAATTTATTTAGGCGCTGTGGCGGGTG	4980
Db	4921	ACCAAGGG	CCCTGACGCGCTCCCGGCG	CCAAATTTATTTAGGCGCTGTGGCGGGTG	4980
QY	4981	GCTGCTGA	GAGGTACGTGAGGTTAC	CGGGTGGGGATTTCCACTACGTGAC	5040
Db	4981	GCTGCTGA	GAGGTACGTGAGGTTAC	CGGGTGGGGATTTCCACTACGTGAC	5040

QY	6121	CTGGGAGAGAGGTCACCTTTGACAGACTGAGGTCTTGGAGGACCACTACCGGGAC	6180	Db	7201	TCCTGGCTAGGCAACATCATGTATGCGCCACCTTGTGGGCAAGGATGATCCTGATG	7260
Db	6121	CTGGGAGAGAGGTCACCTTTGACAGACTGAGGTCTTGGAGGACCACTACCGGGAC	6180	QY	7261	ACTCATTTCTTCCATCTTCTAGCTCAGAAACAACTTGAAAAAGCCCTAGATTGTGAC	7320
QY	6181	GTGCTCAAGGAGTGAAGGCGAAGCGTCCACAGTTAAGGCTAAACTTCTATCCGTGGAG	6240	Db	7261	ACTCATTTCTTCCATCTTCTAGCTCAGAAACAACTTGAAAAAGCCCTAGATTGTGAC	7320
Db	6181	GTGCTCAAGGAGTGAAGGCGAAGCGTCCACAGTTAAGGCTAAACTTCTATCCGTGGAG	6240	QY	7321	ATCTACGGGGCTGTACTTCCATTTAGCCACTTGACCTACCTCAGATCATTTCAACGACTC	7380
QY	6241	GAAGCTGTAACTGAGCGCCGCCACATTTGGCCAGATCAATAATTGGCTATGGGGCAAG	6300	Db	7321	ATCTACGGGGCTGTACTTCCATTTAGCCACTTGACCTACCTCAGATCATTTCAACGACTC	7380
Db	6241	GAAGCTGTAACTGAGCGCCGCCACATTTGGCCAGATCAATAATTGGCTATGGGGCAAG	6300	QY	7381	CATGCCCTTAGCGCATTTTCACTCCATAGTTACTCTCCAGGTGAGATCAATAGGGTGGCT	7440
QY	6301	GACGTCGGAACTTATCCAGCAAGCGGTTAACHACATCCGCTCGTGTGGAAGACTTG	6360	Db	7381	CATGCCCTTAGCGCATTTTCACTCCATAGTTACTCTCCAGGTGAGATCAATAGGGTGGCT	7440
Db	6301	GACGTCGGAACTTATCCAGCAAGCGGTTAACHACATCCGCTCGTGTGGAAGACTTG	6360	QY	7441	TCATGCCCTCAGAAACCTTGGGGTACCGCCCTTGGAGTCTGGAGACATCGGGCCAGAAAT	7500
QY	6361	CTGGAAGACACTGAGACCAATTCACACACCACTCATGGCAAAAAATGAGGTTTCTGC	6420	Db	7441	TCATGCCCTCAGAAACCTTGGGGTACCGCCCTTGGAGTCTGGAGACATCGGGCCAGAAAT	7500
Db	6361	CTGGAAGACACTGAGACCAATTCACACACCACTCATGGCAAAAAATGAGGTTTCTGC	6420	QY	7501	GTCCGCGCTAGGCTACTGTCCAGGGGGAGGGTGCACCTTGTGGCAAGTACCTCTTC	7560
QY	6421	GTCCAAACAGAGAGGGGGCGGCAAGCGAGTCCGCTTATCGTATTCAGATTGGGG	6480	Db	7501	GTCCGCGCTAGGCTACTGTCCAGGGGGAGGGTGCACCTTGTGGCAAGTACCTCTTC	7560
Db	6421	GTCCAAACAGAGAGGGGGCGGCAAGCGAGTCCGCTTATCGTATTCAGATTGGGG	6480	QY	7561	AACCTGGGAGTGAAGACCAAGCTCAAACTCACTCCAAATCCCGGCTGCGTCCAGTTGGAT	7620
QY	6481	GTTCGTGTGCGAGAAATGSCCCTTTACGATGTGCTCCACCTCCCTCAGGCCGTG	6540	Db	7561	AACCTGGGAGTGAAGACCAAGCTCAAACTCACTCCAAATCCCGGCTGCGTCCAGTTGGAT	7620
Db	6481	GTTCGTGTGCGAGAAATGSCCCTTTACGATGTGCTCCACCTCCCTCAGGCCGTG	6540	QY	7621	TTATCCAGCTGTTCGTTGCTGTTACAGCGGGGAGACATATATCAGACCTGTCTGT	7680
QY	6541	ATGGGCTCTTCATACGATTCGATCTCTCTGGACAGCGGTGAGTTCCTGGTGAAT	6600	Db	7621	TTATCCAGCTGTTCGTTGCTGTTACAGCGGGGAGACATATATCAGACCTGTCTGT	7680
Db	6541	ATGGGCTCTTCATACGATTCGATCTCTCTGGACAGCGGTGAGTTCCTGGTGAAT	6600	QY	7681	GCCGACCCCGCTGGTTTCACTGGTGCCTTACTTCTTCTGTAGGGTAGGCATCTAT	7740
QY	6601	GCTTGAAGCGAAGAAATGCCCTATGCGCTTCCGATGATGACACCCGCTGTTTGA	6660	Db	7681	GCCGACCCCGCTGGTTTCACTGGTGCCTTACTTCTTCTGTAGGGTAGGCATCTAT	7740
Db	6601	GCTTGAAGCGAAGAAATGCCCTATGCGCTTCCGATGATGACACCCGCTGTTTGA	6660	QY	7741	CTACTCCCAACCGATGAACGGGAGCTAAACACTCCAGGCCAAATAGGCCATCTCTTTT	7800
QY	6661	ACGCTCAGTGAAGTACATCCGTTGAGGAGTCAATCTACCAATGTTGACTTGGCC	6720	Db	7741	CTACTCCCAACCGATGAACGGGAGCTAAACACTCCAGGCCAAATAGGCCATCTCTTTT	7800
Db	6661	ACGCTCAGTGAAGTACATCCGTTGAGGAGTCAATCTACCAATGTTGACTTGGCC	6720	QY	7801	TTTTCCCTT	7860
QY	6721	CCGGAAGCCAGACAGCCATAGGTCCTCACAGAGCGGCTTTACATCGGGGGCCCGCTG	6780	Db	7801	TTTTCCCTT	7860
Db	6721	CCGGAAGCCAGACAGCCATAGGTCCTCACAGAGCGGCTTTACATCGGGGGCCCGCTG	6780	QY	7861	TTTTTCTCTTTTTTTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	7920
QY	6781	ACTAATTTAAAGGGCAGAACTGCGGCTATCGCGGTGCGCGCGAGCGGTGACTGACG	6840	Db	7861	TTTTTCTCTTTTTTTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	7920
Db	6781	ACTAATTTAAAGGGCAGAACTGCGGCTATCGCGGTGCGCGCGAGCGGTGACTGACG	6840	QY	7921	TAGCTGTGAAGGTCGCTGAGCGGCTTGAAGGAGTGTGATGATGATGATGATGATGATG	7980
QY	6841	ACCAGCTGCGGTAAATACCTTCACTGTTACTTGAAGCGCGCTGCGGCTGCGAGCTGCG	6900	Db	7921	TAGCTGTGAAGGTCGCTGAGCGGCTTGAAGGAGTGTGATGATGATGATGATGATGATG	7980
Db	6841	ACCAGCTGCGGTAAATACCTTCACTGTTACTTGAAGCGCGCTGCGGCTGCGAGCTGCG	6900	QY	7981	AGATCAAGTACT 7992	
QY	6901	AAGCTCCAGGACTGACAGATGCTGATGCGGAGACGACCTTGTCTGTTATCTGTGAAGC	6960	Db	7981	AGATCAAGTACT 7992	
Db	6901	AAGCTCCAGGACTGACAGATGCTGATGCGGAGACGACCTTGTCTGTTATCTGTGAAGC	6960				
QY	6961	CGCGGAGCCCAAGAGGACGAGGCGCTTACGAGGCTTACGAGGCTATGACTAGATAC	7020				
Db	6961	CGCGGAGCCCAAGAGGACGAGGCGCTTACGAGGCTTACGAGGCTATGACTAGATAC	7020				
QY	7021	TCTGCCCCCTTGGGAGCCCGCCCAACACAGATTAAGACTTGGAGTTGATAACATCATGC	7080				
Db	7021	TCTGCCCCCTTGGGAGCCCGCCCAACACAGATTAAGACTTGGAGTTGATAACATCATGC	7080				
QY	7081	TCCTCCCAATGTGTCAGTCCGCGCAGATGTCATCTGGCAAAAGGGTGTACTATCTACCCGT	7140				
Db	7081	TCCTCCCAATGTGTCAGTCCGCGCAGATGTCATCTGGCAAAAGGGTGTACTATCTACCCGT	7140				
QY	7141	GACCCACCAACCCCTTGGCGGGCTGCGTGGAGACAGCTACACACACTCCAGTCAAT	7200				
Db	7141	GACCCACCAACCCCTTGGCGGGCTGCGTGGAGACAGCTACACACACTCCAGTCAAT	7200				
QY	7201	TCCTGGCTAGGCAACATCATGATGATGCGGCCACCTTGTGGGCAAGGATGATCCTGATG	7260				

RESULT 7
ABK91435
ID ABK91435 standard; DNA; 10690 BP.
XX
AC ABK91435;
XX
XX
XX
XX
15-NOV-2002 (first entry)
Hepatitis C virus vector construct pHCVNeo.17m2.
HCV; ss; pHCVNeo.17m2; adaptive mutation; liver failure; cirrhosis;
hepatocellular carcinoma; NS3; NS5; encephalomyocarditis virus; EMCV;
internal ribosome entry site; IRES; NSSA; HCV replication; mutant.
Hepatitis C virus.
Encephalomyocarditis virus.
Escherichia coli.

OS Enterobacteria phage T7.
 XX Synthetic.
 XX
 PH Key Location/Qualifiers
 FT 5'UTR 1..341
 FT /tag= a
 FT CDS 342..1181
 FT /tag= b
 FT /product= "Core-neo fusion protein"
 FT misc_signal 1190..1800
 FT /tag= c
 FT /label= IRES
 FT /note= "Internal ribosome entry site from EMCV"
 FT CDS 1801..7758
 FT /tag= d
 FT /product= "Polyprotein"
 FT /note= "Comprising NS3, NS4A, NS4B, NS5A and NS5B"
 FT mutation replace(5243,C)
 FT /tag= e
 FT 3'UTR 7759..7991
 FT /tag= f
 FT misc_feature 7992..10690
 FT /tag= g
 FT /note= "Plasmid derived sequences"
 XX
 PN WO200259321-A2.
 XX
 XX 01-AUG-2002.
 XX
 XX 16-JAN-2002; 2002WO-EP000526.
 PF
 XX 23-JAN-2001; 2001US-0263479P.
 PR
 XX (RICE-) IST RICERCHIE BIOL MOLECOLARE ANGELETTI.
 PA
 PI De Francesco R, Migliaccio G, Paonessa G;
 XX WPI; 2002-599793/64.
 XX
 PT New Hepatitis C virus (HCV) replicons comprising altered HCV NS3 or HCV
 PT NS5 encoding region, or encephalomyocarditis virus (EMCV) internal
 PT ribosome entry site (IRES) region, useful in studying HCV replication and
 PT expression.
 XX
 PS Claim 16; Page; 69pp; English.
 XX
 CC The invention relates to nucleic acid molecules comprising altered HCV
 CC NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV)
 CC internal ribosome entry site (IRES) region coding for one or more NS3,
 CC NS5A, or EMCV IRES mutations, respectively. The location of the mutations
 CC are detailed in the specification. Also included are (1) an expression
 CC vector comprising a nucleotide sequence coding for the altered nucleic
 CC acids, which is transcriptionally coupled to an exogenous promoter; (2) a
 CC recombinant cell human hepatoma cell comprising the altered nucleic acids
 CC ; (3) a recombinant cell produced by introducing into a human hepatoma
 CC cell the altered nucleic acids; (4) producing an HCV (hepatitis C virus)
 CC replicon enhanced cell or which containing a functional HCV replicon; (5)
 CC an HCV replicon enhanced cells made in the method; and (6) measuring the
 CC ability of a compound to affect HCV activity. The HCV replicons and HCV
 CC replicon enhanced cells are useful in studying HCV replication and
 CC expression, and HCV and host cell interactions, producing HCV RNA and
 CC proteins, and providing a system for measuring the ability of a compound
 CC to modulate one or more HCV activities e.g. to discover drugs which may
 CC treat HCV mediated diseases such as liver failure, cirrhosis and
 CC hepatocellular carcinoma. The present sequence is an HCV based vector
 CC pHCVneo.17 mutant of the invention. Note: The present sequence is not
 CC shown in the specification but was created by the indexer using the HCV
 CC vector sequence appearing as ABK91412 and the information in Claim 16
 XX
 SQ Sequence 10690 BP; 2334 A; 3044 C; 2908 G; 2404 T; 0 U; 0 Other;
 Query Match 99.9%; Score 7984; DB 6; Length 10690;
 Best Local Similarity 99.9%; Pred. No. 0;

		Matches	7987;	Conservative	0;	Mismatches	5;	Indels	0;	Gaps	0;
QY	1	GCAGCCCCCGATTGGGGCGACACTCCACCATAGATCACTCCCTCTGTGAGAACTACTG	60								
DB	1	GCAGCCCCCGATTGGGGCGACACTCCACCATAGATCACTCCCTCTGTGAGAACTACTG	60								
QY	61	TCATTACGACAGAAAGCGTCTAGCCATGGCGTTAGTATGATGTCGTGAGCTCCAGAAC	120								
DB	61	TCATTACGACAGAAAGCGTCTAGCCATGGCGTTAGTATGATGTCGTGAGCTCCAGAAC	120								
QY	121	CCCCCTCCCGGAGAGCCATAGTGGTCTCGGAAACGGTGTAGTACACCGAATTCGAG	180								
DB	121	CCCCCTCCCGGAGAGCCATAGTGGTCTCGGAAACGGTGTAGTACACCGAATTCGAG	180								
QY	181	GACGACCGGTCCTTTCTTGGATCAAGCCGCTCAATGCTCGAGATTGGCGTGCCTCC	240								
DB	181	GACGACCGGTCCTTTCTTGGATCAAGCCGCTCAATGCTCGAGATTGGCGTGCCTCC	240								
QY	241	GCGAGACTGTAGCCGAGTAGTGTGGTTCGGAAGAGCCCTTGTGTACTGCTGTATAGG	300								
DB	241	GCGAGACTGTAGCCGAGTAGTGTGGTTCGGAAGAGCCCTTGTGTACTGCTGTATAGG	300								
QY	301	GTGCTTCGAGTGCCTCGGAGGTCTCGTAGACCGTGCACCATGACGACGATCCTTAAC	360								
DB	301	GTGCTTCGAGTGCCTCGGAGGTCTCGTAGACCGTGCACCATGACGACGATCCTTAAC	360								
QY	361	CTCAAGAAAAACCAAGAGCGCGCCATGATTGAACAAGATGGATTGACGAGGTTCTC	420								
DB	361	CTCAAGAAAAACCAAGAGCGCGCCATGATTGAACAAGATGGATTGACGAGGTTCTC	420								
QY	421	CGGCGCTTGGTGGAGAGGCTATTGGCTATGATGCTGGGCAACAGACAAATCGGCTGCT	480								
DB	421	CGGCGCTTGGTGGAGAGGCTATTGGCTATGATGCTGGGCAACAGACAAATCGGCTGCT	480								
QY	481	CTGATGCGGCGGTTCCGGCTGTGAGAGGCTATTGGCTATGATGCTGGGCAACAGAC	540								
DB	481	CTGATGCGGCGGTTCCGGCTGTGAGAGGCTATTGGCTATGATGCTGGGCAACAGAC	540								
QY	541	ACTGTCCGTCCTGTAATGAACTGACGACGAGGCGCGGCTATCGTGGTGGCCCA	600								
DB	541	ACTGTCCGTCCTGTAATGAACTGACGACGAGGCGCGGCTATCGTGGTGGCCCA	600								
QY	601	CGAGCGGCTTCTTCCGAGCTGTGCTGCACTGTAAGCGGGAAGGAGCTGGC	660								
DB	601	CGAGCGGCTTCTTCCGAGCTGTGCTGCACTGTAAGCGGGAAGGAGCTGGC	660								
QY	661	TGCTATTGGCGGAGTGCCTGGGCGAGATCTCTCTCATCTCATCTGCTTCTTCTGCGG	720								
DB	661	TGCTATTGGCGGAGTGCCTGGGCGAGATCTCTCTCATCTCATCTGCTTCTTCTGCGG	720								
QY	721	AAGTATCCATCATGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCC	780								
DB	721	AAGTATCCATCATGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCC	780								
QY	781	CATTGACCAACCAAGGAAACATCGATCAGGAGCAGTACTCGATGGAAGCGCGTC	840								
DB	781	CATTGACCAACCAAGGAAACATCGATCAGGAGCAGTACTCGATGGAAGCGCGTC	840								
QY	841	TTGTTCGATCAGGATGATCTGGACGAGAGCATCAGGGCTCGGCCAGCGGACTTTTCG	900								
DB	841	TTGTTCGATCAGGATGATCTGGACGAGAGCATCAGGGCTCGGCCAGCGGACTTTTCG	900								
QY	901	CCAGGCTCAAGGCGCGCATGCTGGACGAGAGCATCAGGGCTCGGCCAGCGGACTTTTCG	960								
DB	901	CCAGGCTCAAGGCGCGCATGCTGGACGAGAGCATCAGGGCTCGGCCAGCGGACTTTTCG	960								
QY	961	GCTTCCGGAATATCATGTTGGAAATGCGCGCTTTTCTGGATTCATTCGACTGTGCGCGC	1020								
DB	961	GCTTCCGGAATATCATGTTGGAAATGCGCGCTTTTCTGGATTCATTCGACTGTGCGCGC	1020								
QY	1021	TGGGTGTGCGGACCGCTATCAGGACATAGCTTGGCTACCGCTGATATTGCTGAAGAGC	1080								
DB	1021	TGGGTGTGCGGACCGCTATCAGGACATAGCTTGGCTACCGCTGATATTGCTGAAGAGC	1080								

QY	1081	TTGGCGGGAATGGGCTGAACGCTTCCTCGTCTTTACGGTATCGCGCTCCCGATTGCG	1140	QY	2161	GGCGACAGAGGGGAGCTACTCTCCCGCAGGCGCCGCTCTCTACTTTGAAGGGCTCTTCG	2220
Db	1081	TTGGCGGGAATGGGCTGAACGCTTCCTCGTCTTTACGGTATCGCGCTCCCGATTGCG	1140	Db	2161	GGCGACAGAGGGGAGCTACTCTCCCGCAGGCGCCGCTCTCTACTTTGAAGGGCTCTTCG	2220
QY	1141	AGCGATCGCCTTCTATCGCCTTCTTGACGAGTCTTCTGAGTTTAAACAGACACACACG	1200	QY	2221	GGCGGTCCACTGCTCTGCGCCCTCGGGGACGCTGTGGGCATCTTTCCGGCTGCGGTGTC	2280
Db	1141	AGCGATCGCCTTCTATCGCCTTCTTGACGAGTCTTCTGAGTTTAAACAGACACACACG	1200	Db	2221	GGCGGTCCACTGCTCTGCGCCCTCGGGGACGCTGTGGGCATCTTTCCGGCTGCGGTGTC	2280
QY	1201	GTTCCTCTTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCGCCCTTAACGTTACTGCG	1260	QY	2281	ACCGAGGGGTTGCGAGCGGTGACTTTCTACCCGTCGAGTCTATCGAAACCACTATG	2340
Db	1201	GTTCCTCTTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCGCCCTTAACGTTACTGCG	1260	Db	2281	ACCGAGGGGTTGCGAGCGGTGACTTTCTACCCGTCGAGTCTATCGAAACCACTATG	2340
QY	1261	CGAAGCCCTTGAATAAGCGGCTGCTGCTTTGCTATATGTTATTTTCCACCATATG	1320	QY	2341	CGGTCCCGGCTTTACAGCAAACTCGTCCCTCGGCGGTAACGACAGACATTCAGGTG	2400
Db	1261	CGAAGCCCTTGAATAAGCGGCTGCTGCTTTGCTATATGTTATTTTCCACCATATG	1320	Db	2341	CGGTCCCGGCTTTACAGCAAACTCGTCCCTCGGCGGTAACGACAGACATTCAGGTG	2400
QY	1321	CGGTCTTTTGGCAATGTAGGCGCGGTGCTGCTTTGCTATATGTTATTTTCCACCATATG	1380	QY	2401	GCCCATCTACAGCGCCCTACTGGTAGCGGCAAGAGCACTAAGGTGCCGCTGCGTATGCA	2460
Db	1321	CGGTCTTTTGGCAATGTAGGCGCGGTGCTGCTTTGCTATATGTTATTTTCCACCATATG	1380	Db	2401	GCCCATCTACAGCGCCCTACTGGTAGCGGCAAGAGCACTAAGGTGCCGCTGCGTATGCA	2460
QY	1381	AGGGCTCTTCCCTCTCGCCAAAGGAATGCAAGGTCTGTTGAATGTCTGTGAAGGAACA	1440	QY	2461	GCCCAAGGATATAAGGTCTTGTCTGAAACCGCTCGGCGCCACCCCTAGGTTTCGGG	2520
Db	1381	AGGGCTCTTCCCTCTCGCCAAAGGAATGCAAGGTCTGTTGAATGTCTGTGAAGGAACA	1440	Db	2461	GCCCAAGGATATAAGGTCTTGTCTGAAACCGCTCGGCGCCACCCCTAGGTTTCGGG	2520
QY	1441	GTTCCTCTGGAAGCTTCTTGAAGCAAAACAGCTGTAGGACCCCTTTCAGGAGCGG	1500	QY	2521	GGGTATATCTTAAGSCACATGGTATCGACCTTAACATCAGAAACCGGGGTAAAGCAATC	2580
Db	1441	GTTCCTCTGGAAGCTTCTTGAAGCAAAACAGCTGTAGGACCCCTTTCAGGAGCGG	1500	Db	2521	GGGTATATCTTAAGSCACATGGTATCGACCTTAACATCAGAAACCGGGGTAAAGCAATC	2580
QY	1501	AAACCCCACTGGGAGAGGTGCTCTGCGGCAAAAGCCACGCTGTATAGATACACT	1560	QY	2581	ACCAAGGTGCCCTCATCAGTACTCCACCTATGAGTGCCTCAACTGACTCGACCACT	2640
Db	1501	AAACCCCACTGGGAGAGGTGCTCTGCGGCAAAAGCCACGCTGTATAGATACACT	1560	Db	2581	ACCAAGGTGCCCTCATCAGTACTCCACCTATGAGTGCCTCAACTGACTCGACCACT	2640
QY	1561	GCAAGGCGGCAAAACCCAGTGCACAGTGTGAGTTGATAGTTGTGAAAGAGTCAAA	1620	QY	2641	TCGTGGGCGGCTATGACATATAATATGATGAGTGCCACTCAACTGACTCGACCACT	2700
Db	1561	GCAAGGCGGCAAAACCCAGTGCACAGTGTGAGTTGATAGTTGTGAAAGAGTCAAA	1620	Db	2641	TCGTGGGCGGCTATGACATATAATATGATGAGTGCCACTCAACTGACTCGACCACT	2700
QY	1621	TGGCTCTCTAAGGCTATTAACAAAGGGCTGAGGATGCCAGAGTACCCCATCTG	1680	QY	2701	ATCTGGGCATCGGCACAGTCTCTGCAACAAAGCGGAGAGCGCTGGAGCGGCTCGTCTG	2760
Db	1621	TGGCTCTCTAAGGCTATTAACAAAGGGCTGAGGATGCCAGAGTACCCCATCTG	1680	Db	2701	ATCTGGGCATCGGCACAGTCTCTGCAACAAAGCGGAGAGCGCTGGAGCGGCTCGTCTG	2760
QY	1681	ATGGGATCTGATCTGGGCTCTGGTGCACATGTTTACATGTTTGTAGTTCGAGTTTAAA	1740	QY	2761	CTGCCACCGCTACGCTCGGGATCGGTACCGTGCCACATCCAAACATCGAGGAGGTG	2820
Db	1681	ATGGGATCTGATCTGGGCTCTGGTGCACATGTTTACATGTTTGTAGTTCGAGTTTAAA	1740	Db	2761	CTGCCACCGCTACGCTCGGGATCGGTACCGTGCCACATCCAAACATCGAGGAGGTG	2820
QY	1741	AAGCTCTAGGCCCCCGAACCAAGGAGCGTGTTCCTTTGAAAAACAAGATATACC	1800	QY	2821	GCTCTGTCCAGCACTGGAGAAATCCCTTTTATGGCAAGCCATCCCATCGAGACCATC	2880
Db	1741	AAGCTCTAGGCCCCCGAACCAAGGAGCGTGTTCCTTTGAAAAACAAGATATACC	1800	Db	2821	GCTCTGTCCAGCACTGGAGAAATCCCTTTTATGGCAAGCCATCCCATCGAGACCATC	2880
QY	1801	ATGGGCGCTATTAAGGCTACTCCACAGACGCGAGGCTACTTGGCTGCATCATCACT	1860	QY	2881	AAGGGGGAGGACCTCATTTTCTGCCATTCAGAGAAATGTGATGAGTTCGCGG	2940
Db	1801	ATGGGCGCTATTAAGGCTACTCCACAGACGCGAGGCTACTTGGCTGCATCATCACT	1860	Db	2881	AAGGGGGAGGACCTCATTTTCTGCCATTCAGAGAAATGTGATGAGTTCGCGG	2940
QY	1861	AGCTCAGAGCGGAGACAGAACAGGTGCGAGGGAGGTCCAGGTGCTCCACCGCA	1920	QY	2941	AAGTGTCCGGCTCGGACTCAATGCTGTAGCATATTTACCGGGCTTGTATGATCCGTC	3000
Db	1861	AGCTCAGAGCGGAGACAGAACAGGTGCGAGGGAGGTCCAGGTGCTCCACCGCA	1920	Db	2941	AAGTGTCCGGCTCGGACTCAATGCTGTAGCATATTTACCGGGCTTGTATGATCCGTC	3000
QY	1921	ACACAACTTTCTTGGCGACTCGCTCAATGGCGGTGTGTGGACTGTCTATCATGTGTC	1980	QY	3001	ATACCAACTAGCGGAGACGCTATTGTCTGTAGCAACGAGCGCTCTAATGACGGCTTTACC	3060
Db	1921	ACACAACTTTCTTGGCGACTCGCTCAATGGCGGTGTGTGGACTGTCTATCATGTGTC	1980	Db	3001	ATACCAACTAGCGGAGACGCTATTGTCTGTAGCAACGAGCGCTCTAATGACGGCTTTACC	3060
QY	1981	GGCTCAAGACCTTTCGCGCCCAAGGGCCCAATCACCACCAATGTACCAATGTGGAC	2040	QY	3061	GGCGATTTGACACTGAGTGTGACTGCAATGATGTGTACCCAGACAGTTCGACTTCAGC	3120
Db	1981	GGCTCAAGACCTTTCGCGCCCAAGGGCCCAATCACCACCAATGTACCAATGTGGAC	2040	Db	3061	GGCGATTTGACACTGAGTGTGACTGCAATGATGTGTACCCAGACAGTTCGACTTCAGC	3120
QY	2041	CAGGACCTCTGCGCTGGCAAGCGCCCGCGGGCGGCTTCTTGAACACCATGCACCTGC	2100	QY	3121	CTGGAACCGGACCTTCACTTGTAGAGACGACCGCTGCCAAGACGCGGTGTCAACGCTCG	3180
Db	2041	CAGGACCTCTGCGCTGGCAAGCGCCCGCGGGCGGCTTCTTGAACACCATGCACCTGC	2100	Db	3121	CTGGAACCGGACCTTCACTTGTAGAGACGACCGCTGCCAAGACGCGGTGTCAACGCTCG	3180
QY	2101	GGCAGCTCGGACCTTTACTTGGTCAAGGAGATCCGATGCTCATCTCGGTGCGCGCGG	2160	QY	3181	CAGCGGCGAGCGAGGACTGGTAGGGCAGGATGGGCAATTTACAGGTTTGTGACTCCAGGA	3240
Db	2101	GGCAGCTCGGACCTTTACTTGGTCAAGGAGATCCGATGCTCATCTCGGTGCGCGCGG	2160	Db	3181	CAGCGGCGAGCGAGGACTGGTAGGGCAGGATGGGCAATTTACAGGTTTGTGACTCCAGGA	3240
				QY	3241	GAACGGCCCTCGGGCATGTTGATTCTCTGCTGTGCGAGTCTATGACGCGGGCTGT	3300

[illegible]

Db 361 CTCAAGAGAAACCAAGGGCGCCATGATTGAACAAGATGGATTGACAGCAGTTCTC 420
 Qy 421 CGGCGCTTGGGTGGAGAGGCTATTGGCTATGACTGGGCAACAAGACAATCGGCTGCT 480
 Db 421 CGGCGCTTGGGTGGAGAGGCTATTGGCTATGACTGGGCAACAAGACAATCGGCTGCT 480
 Qy 481 CTGATGCGCGCGTGTTCGGCTGTGACGCGAGGGCGCGCGTTCCTTTTGTCAAGACCG 540
 Db 481 CTGATGCGCGCGTGTTCGGCTGTGACGCGAGGGCGCGCGTTCCTTTTGTCAAGACCG 540
 Qy 541 ACCTGTCCGGTCCCTGAATGAATGACGAGGAGGCGGCGCTATCTGCTGGCTGGCCA 600
 Db 541 ACCTGTCCGGTCCCTGAATGAATGACGAGGAGGCGGCGCTATCTGCTGGCTGGCCA 600
 Qy 601 CGAGCGGCGTTCCTTTCGCGCAGCTGTGCTCGACGTTGTCACTGAACGCGGAAGGGACTGGC 660
 Db 601 CGAGCGGCGTTCCTTTCGCGCAGCTGTGCTCGACGTTGTCACTGAACGCGGAAGGGACTGGC 660
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 Db 841 TTGTCGATCAGGATGATCTGAGCAAGAGACATCAGGGGCTCGCGCAGCGAAGCTGTTCCG 900
 Qy 901 CCAGGCTCAAGCGCGCATGCGCGAGGAGATCTCGTCTGATGACCAATGGCGATGCTCCT 960
 Db 901 CCAGGCTCAAGCGCGCATGCGCGAGGAGATCTCGTCTGATGACCAATGGCGATGCTCCT 960
 Qy 961 GCTTTCGGAATATCATGTTGGAATATGGCGCTTTTCTGGAATCATCGACTGTGGCGCGC 1020
 Db 961 GCTTTCGGAATATCATGTTGGAATATGGCGCTTTTCTGGAATCATCGACTGTGGCGCGC 1020
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 Db 1021 TGGGTGTGGGACCCGCTATCAGGACATAGCGTTGGCTACCGTGATATTTGCTGAAGAGC 1080
 Qy 1081 TTGGCGCGAATGCGGCTGACCGTCTCTCTGCTTTTACGATATCGCGCTCCCGATTGCG 1140
 Db 1081 TTGGCGCGAATGCGGCTGACCGTCTCTCTGCTTTTACGATATCGCGCTCCCGATTGCG 1140
 Qy 1141 AGCGCATCGCCTTTCTATCGCCTTTCTGACGAGTTCTTCTGAGTTTAAACAGACCAACAG 1200
 Db 1141 AGCGCATCGCCTTTCTATCGCCTTTCTGACGAGTTCTTCTGAGTTTAAACAGACCAACAG 1200
 Qy 1201 GTTTCCTCTAGCGGATCAATTCGCGCTCTCCCTCCCGCTTAACTGCTTACTGGC 1260
 Db 1201 GTTTCCTCTAGCGGATCAATTCGCGCTCTCCCTCCCGCTTAACTGCTTACTGGC 1260
 Qy 1261 CGAAGCGCTTGAATTAAGCGCGGTGTGCTTGTCTATATGTTATTTTCCACCATATTG 1320
 Db 1261 CGAAGCGCTTGAATTAAGCGCGGTGTGCTTGTCTATATGTTATTTTCCACCATATTG 1320
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 Db 1321 CGGTCTTTTGGCAATGAGGCGCGGAACTGGCGCTCTCTCTGAGAGCTTAACTGCTTCT 1380
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 Db 1441 GTTCTCTGGAAGCTTCTTGAAGCAAAACAAAGCTGCTGAGCAGCCCTTTGAGCAGCGG 1500

Qy 1501 AACCCCCACCTGCGCAGAGTGCCTCTGCGGCCAAAAGCCACCGTGTATAGATACACCT 1560
 Db 1501 AACCCCCACCTGCGCAGAGTGCCTCTGCGGCCAAAAGCCACCGTGTATAGATACACCT 1560
 Qy 1561 GCAAAGGCGGCAACCCCACTGCGCAGTGTGAGTTGGATAGTTGTGGAAAGAGTCAAA 1620
 Db 1561 GCAAAGGCGGCAACCCCACTGCGCAGTGTGAGTTGGATAGTTGTGGAAAGAGTCAAA 1620
 Qy 1621 TGGCTCTCTCAAGCGTATTCAACAAGGGGCTGAAGGATGCCCAAGAGTACCCATTTGT 1680
 Db 1621 TGGCTCTCTCAAGCGTATTCAACAAGGGGCTGAAGGATGCCCAAGAGTACCCATTTGT 1680
 Qy 1681 ATGGGATCTGATCTGGGCGCTCGGTGCATGCTTTACATGTTGTTTGTAGTGTAAATA 1740
 Db 1681 ATGGGATCTGATCTGGGCGCTCGGTGCATGCTTTACATGTTGTTTGTAGTGTAAATA 1740
 Qy 1741 AACGCTTAGGCGCCCGGAAACCAAGGGGAGTGGTTTTCTTTGAAAAACAGATATATACC 1800
 Db 1741 AACGCTTAGGCGCCCGGAAACCAAGGGGAGTGGTTTTCTTTGAAAAACAGATATATACC 1800
 Qy 1801 ATGGCGCTTATAGGCGCTTCTCCCAACAGAGCGGAGGCTTACTTTGGCTGCAATCATCACT 1860
 Db 1801 ATGGCGCTTATAGGCGCTTCTCCCAACAGAGCGGAGGCTTACTTTGGCTGCAATCATCACT 1860
 Qy 1861 AGCCTCAAGGCGCGGACAGGAAACAGGTCGAGGGGAGGTCCTTCTCCACCGCA 1920
 Db 1861 AGCCTCAAGGCGCGGACAGGAAACAGGTCGAGGGGAGGTCCTTCTCCACCGCA 1920
 Qy 1921 ACACAACTTTCTCGCGACCTGCTCAATGGCGTGTGTGGACATGTCTATCATGGTGC 1980
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 Qy 1981 GGCTCAAGACCTTTGCGGCGCCAAAGGCGCCAAATCACCCAAATGTACACCAATGTGGAC 2040
 Db 1981 GGCTCAAGACCTTTGCGGCGCCAAAGGCGCCAAATCACCCAAATGTACACCAATGTGGAC 2040
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7981 AGATCAAGTACT 7992
7981 AGATCAAGTACT 7992

RESULT 9
ABK91434
ID ABK91434 standard; DNA; 10690 BP.
XX
AC ABK91434;
XX
DT 15-NOV-2002 (first entry)
XX
DE Hepatitis C virus vector construct pHCVNeo.17m0.
XX
KW HCV; ss; pHCVNeo.17m2; adaptive mutation; liver failure; cirrhosis;
KW hepatocellular carcinoma; NS3; NS5; encephalomyocarditis virus; EMCV;
KW internal ribosome entry site; IRES; NS5A; HCV replication; mutant.
XX
OS Hepatitis C virus.
OS Encephalomyocarditis virus.
OS Escherichia coli.
OS Enterobacteria phage T7.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT 5'UTR 1..341
FT /*tag= a
FT CDS 342..1181
FT /*tag= b
FT /*product= "Core-neo fusion protein"
FT misc_signal 1190..1800
FT /*tag= c
FT /*label= IRES
FT /*note= "Internal ribosome entry site from EMCV"
FT CDS 1801..7758
FT /*tag= d
FT /*product= "Polyprotein"
FT /*note= "Comprising NS3, NS4A, NS4B, NS5A and NS5B"
FT mutation replace(5337,C)
FT /*tag= e
FT 3'UTR 7759..7991
FT /*tag= f
FT misc_feature 7992..10690
FT /*tag= g
FT /*note= "Plasmid derived sequences"
XX
DN WO200259321-A2.
XX
PD 01-AUG-2002.
XX
PF 16-JAN-2002; 2002WO-EP000526.
XX
PR 23-JAN-2001; 2001US-0263479P.
XX
PA (RICE-) IST RICERHE BIOL MOLECOLARE ANGELETTI.
XX
PI De Francesco R, Migliaccio G, Paonessa G;
XX
DR WPI; 2002-599793/64.
XX
PT New Hepatitis C virus (HCV) replicons comprising altered HCV NS3 or HCV
PT NS5 encoding region, or encephalomyocarditis virus (EMCV) internal
PT ribosome entry site (IRES) region, useful in studying HCV replication and
PT expression.
XX
PS Claim 16; Page; 69pp; English.
XX
CC The invention relates to nucleic acid molecules comprising altered HCV
CC NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV)
CC internal ribosome entry site (IRES) region coding for one or more NS3,
CC NS5A, or EMCV IRES mutations, respectively. The location of the mutations
CC are detailed in the specification. Also included are (1) an expression
CC vector comprising a nucleotide sequence coding for the altered nucleic
CC acids, which is transcriptionally coupled to an exogenous promoter; (2) a
CC recombinant cell human hepatoma cell comprising the altered nucleic acids
CC ; (3) a recombinant cell produced by introducing into a human hepatoma
CC cell the altered nucleic acids; (4) producing an HCV (hepatitis C virus)

CC replicon enhanced cell or which containing a functional HCV replicon: (5)
 CC an HCV replicon enhanced cells made in the method; and (6) measuring the
 CC ability of a compound to affect HCV activity. The HCV replicons and HCV
 CC replicon enhanced cells are useful in studying HCV replication and
 CC expression, and HCV and host cell interactions, producing HCV RNA and
 CC proteins, and providing a system for measuring the ability of a compound
 CC to modulate one or more HCV activities e.g. to discover drugs which may
 CC treat HCV mediated diseases such as liver failure, cirrhosis and
 CC hepatocellular carcinoma. The present sequence is an HCV based vector
 CC pHCVneo.17 mutant of the invention. Note: The present sequence is not
 CC shown in the specification but was created by the indexer using the HCV
 CC vector sequence appearing as ABK91412 and the information in Claim 16
 XX
 SQ Sequence 10690 BP; 2335 A; 3044 C; 2908 G; 2403 T; 0 U; 0 Other;

Query Match 99.9%; Score 7984; DB 6; Length 10690;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 7987; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GCCAGCCCCGATTTGGGGGCGACACTCCACATAGATCACTCCCTGTGAGGAATCTACG 60
 DB 1 GCCAGCCCCGATTTGGGGGCGACACTCCACATAGATCACTCCCTGTGAGGAATCTACG 60

QY 61 TCTTCACGAGAAAGCGTCTAGCCATGGCGTTAGTATGATGTCGTGAGCGCTCCAGGAC 120
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 DB 121 CCCCCCTCCCGGAGAGCCATAGTGTCTCGGAAACCGGTGAGTACACCGGAATGCCAG 180

QY 181 GAGACCGGCTCTTTCTTGGATCAACCGCTCAATGCTGAGGATTTGGGGGTGCCCCC 240
 DB 181 GAGACCGGCTCTTTCTTGGATCAACCGCTCAATGCTGAGGATTTGGGGGTGCCCCC 240

QY 241 GCGAGACTGCTAGCCGAGTGTCTGGTTCGGAAGGCTCTGTGCTACTGCTGATAGG 300
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QY 361 CTCAAGAAAAAACAAGGGGCGCCATGATTTGAACAAGATGATGACGAGGTTCTC 420
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DB 781 CATTCGACCAACAAGCGAAACATCGATCGAGCGAGCAGTACTCGGATGGAAGCCGGTC 840

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Qy	4201	GCTTCTGCTTTCGTAGGCGCGGCAATGCTGAGCGGCTGTTGGAGCAGATAGGCTTGG	5281	GCTAAGCCTTAGGCTGGCCAGGGGATCTCCCGCTCTCTGGCCAGCTCATCAGTAGACAG	5340
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Qy	4261	AGGTGCTTGTGATATTTGACAGTTATGAGCAGGGGTGCGAGCGCGCTCGTGGCC	5341	CTGTCTGCGCTTCTTGAAGCAACATGCACTACCGCTCATGACTCCCGGACGCTGAC	5400
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Db	4441	GTGGGCCAGGGGAGGGGCTGTGACGTGATGAACCGGCTGATAGCTTTCGCTTCGGG	5521	AGGGAAGTATCGTTCCGCGGAGATCTCGCGAGGTCAGGAAATTTCCCTCGAGCGATG	5580
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Qy	4561	CAGATCCTCTAGTCTTACCATCACTCAGCTGCTGAAGGCTTCCACAGTGGATCAAC	5641	TAGTCTCTCTAGTGTGTAACACGCGGTTCATTTGCGCCCTCGCAGCGCTTCCGATACCA	5700
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QY 6901 AAGCTCAGGACTGCAAGTGTGCTATGCGGAGACGACCTTGTCTGTTATCTGTGAAGC 6960
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QY 6901 AAGCTCAGGACTGCAAGTGTGCTATGCGGAGACGACCTTGTCTGTTATCTGTGAAGC 6960
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QY 6961 GCGGGACCCAGAGGACGAGCGGCTAGCGGCTTACGGGCTTACGGAGGCTATGACTAGATAC 7020
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Db |||||
7981 AGATCAAGTACT 7992
Db |||||
RESULT 10
AAA98968
ID AAA98968 standard; DNA; 7989 BP.
XX
AC AAA98968;
XX
DT 08-FEB-2001 (first entry)
XX
DE Hepatitis C virus DNA fragment SEQ ID NO: 4.
XX
KW Cell culture; therapy; infection; vaccine; diagnosis; gene therapy; ds.
XX
OS Hepatitis C virus.
XX
PN DE19915178-Al.
XX
PD 05-OCT-2000.
XX
PF 03-APR-1999; 99DE-01015178.
XX
PR 03-APR-1999; 99DE-01015178.
XX
PA (UTMA-) UNIV MAINZ GUTENBERG JOHANNES.
XX
PI Bartenschlager R;
XX
DR WPI; 2000-629140/61.
XX
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Cell culture system for hepatitis C virus, useful e.g. in screening for therapeutic agents, comprises human hepatoma cells containing a viral RNA construct that includes a selectable gene.

Claim 8; Page 37-43; 58pp; German.

This invention describes a novel Hepatitis C virus (HCV) cell culture system comprising human hepatoma cells that contain an integrated HCV-RNA construct (I). (I) contains the HCV-specific RNA segments 5'-NTR (non-translated region), NS (non-structural), NS4A, NS4B, NS5A, NS5B and 3'-NTR, and a selectable (marker) gene (II). The cell cultures, and/or (I), are used to prepare, evaluate and/or test therapeutic and/or diagnostic agents for HCV infections, and to prepare vaccines against HCV infection (particularly preparation of attenuated HCV). The can also be used for preparation of a liver-specific delivery system for gene therapy, and to identify cells permissive for HCV replication. Virus RNA replicates autonomously in and with high efficiency in this cellular system, so that variations in replication rates can be measured (for screening antiviral agents) quantitatively or qualitatively, using standard laboratory equipment. Efficient replication of HCV RNA is only achieved when the specified RNA segments are present and when the transfected cells are maintained under permanent selection pressure

Sequence 7989 BP; 1647 A; 2368 C; 2243 G; 1731 T; 0 U; 0 Other;

Query Match 99.9%; Score 7982.6; DB 3; Length 7989;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 7985; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY	1	GCACGCCCCGATTGGGGCGACACATCCACCATAGATCACTCCCTGTGAGGAATCTACTG	60
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QY	61	TCTTACGAGAAAGCGTCTAGCCATGGCGTTAGTATAGTGTCTGTCGAGCCCTCCAGGAC	120
DB	61	TCTTACGAGAAAGCGTCTAGCCATGGCGTTAGTATAGTGTCTGTCGAGCCCTCCAGGAC	120
QY	121	CCCCCTCCCGGAGAGCCATAGTGTCTGCGAAACCGGTGAGTACACCGGAATGCCAG	180
DB	121	CCCCCTCCCGGAGAGCCATAGTGTCTGCGAAACCGGTGAGTACACCGGAATGCCAG	180
QY	181	GACGACCGGTCTCTTTTGGATCAACCCCGCTCAATGCTGGAGATTGGGGGTGCCCCC	240
DB	181	GACGACCGGTCTCTTTTGGATCAACCCCGCTCAATGCTGGAGATTGGGGGTGCCCCC	240
QY	241	GCAGACTGTAGCCGAGTAGTGTGGTTCGGAAGAGCCCTTGTGGTACTGTGCTGATAGG	300
DB	241	GCAGACTGTAGCCGAGTAGTGTGGTTCGGAAGAGCCCTTGTGGTACTGTGCTGATAGG	300
QY	301	GTGCTTGGAGTCCCGGGAGGTCTGTAGACCGGTGACCATGACCAAGATCCCTAAAC	360
DB	301	GTGCTTGGAGTCCCGGGAGGTCTGTAGACCGGTGACCATGACCAAGATCCCTAAAC	360
QY	361	CTCAAGAGAAAACCAAGAGCGCGCCATGATTGAACAAGATGGATTGCACGAGTTCTC	420
DB	361	CTCAAGAGAAAACCAAGAGCGCGCCATGATTGAACAAGATGGATTGCACGAGTTCTC	420
QY	421	CGGCGGCTTGGGTGGAGAGGCTATTCCGGCTATGATCTGGGCAACAGACAAATCGGCTGCT	480
DB	421	CGGCGGCTTGGGTGGAGAGGCTATTCCGGCTATGATCTGGGCAACAGACAAATCGGCTGCT	480
QY	481	CTGATCCGCGGTCTCCGGCTGTACGCGAGGGCGCCCGTTCTTTTGTCAAGACCG	540
DB	481	CTGATCCGCGGTCTCCGGCTGTACGCGAGGGCGCCCGTTCTTTTGTCAAGACCG	540
QY	541	ACCTGTCCGGTCCCTGAATGAATCTGACGAGGAGCGCGGCTATCGTGGCTGGCCA	600
DB	541	ACCTGTCCGGTCCCTGAATGAATCTGACGAGGAGCGCGGCTATCGTGGCTGGCCA	600
QY	601	CGACGGCGTCTTGGCAGCTGTCTGACGTTGTCACTGAGCGGAGGAGGACTGGC	660
DB	601	CGACGGCGTCTTGGCAGCTGTCTGACGTTGTCACTGAGCGGAGGAGGACTGGC	660

QY	661	TGCTATTGGCGAAGTGCCTGGGCGAGGATCTCTGTGTATCTCACTTCTCTCTGCGGAGA	720
DB	661	TGCTATTGGCGAAGTGCCTGGGCGAGGATCTCTGTGTATCTCACTTCTCTCTGCGGAGA	720
QY	721	AAGTATCCATCATGGCTGATCAATGCGCGCGCTGCATACGCTTGCATCGGCTACTGCG	780
DB	721	AAGTATCCATCATGGCTGATCAATGCGCGCGCTGCATACGCTTGCATCGGCTACTGCG	780
QY	781	CATTTCGACCAACCAAGCGAAACATCGCATCGAGCGAGCAGTACTCGATGGAAGCGGTC	840
DB	781	CATTTCGACCAACCAAGCGAAACATCGCATCGAGCGAGCAGTACTCGATGGAAGCGGTC	840
QY	841	TTTTCGATCAGGATGATCTGACGAGAGCATCAGGGCTCCGCGAGCCGCACTGTTCCG	900
DB	841	TTTTCGATCAGGATGATCTGACGAGAGCATCAGGGCTCCGCGAGCCGCACTGTTCCG	900
QY	901	CCAGCTCAAGCGCGCATGCGCGAGGAGTCTCTGTCGACCCATGCGATGCGTTC	960
DB	901	CCAGCTCAAGCGCGCATGCGCGAGGAGTCTCTGTCGACCCATGCGATGCGTTC	960
QY	961	GCTTCCCGAATATCATGTGTGAAATGGCGCTTTTCTGGATTTCATCGACTGTGGCGGC	1020
DB	961	GCTTCCCGAATATCATGTGTGAAATGGCGCTTTTCTGGATTTCATCGACTGTGGCGGC	1020
QY	1021	TGGGTGTGGCGACCGCTATCAGGACATAGCGTGTGGCTACCGTGATTTGCTGAAGGC	1080
DB	1021	TGGGTGTGGCGACCGCTATCAGGACATAGCGTGTGGCTACCGTGATTTGCTGAAGGC	1080
QY	1081	TTGGCGGCGAATGGGCTGACCGCTTCTGCTTACGGTATCGCGCTCCGATTCGC	1140
DB	1081	TTGGCGGCGAATGGGCTGACCGCTTCTGCTTACGGTATCGCGCTCCGATTCGC	1140
QY	1141	AGCGCATCGCTTCTATCGCTTCTTTCGAGTTCCTTTCGAGTTTAAACAGACCAACG	1200
DB	1141	AGCGCATCGCTTCTATCGCTTCTTTCGAGTTCCTTTCGAGTTTAAACAGACCAACG	1200
QY	1201	GTTTCCCTCTAGCGGATCAATTCGCGCCCTTCCCTCCCGCCCTTACGTTACTGCG	1260
DB	1201	GTTTCCCTCTAGCGGATCAATTCGCGCCCTTCCCTCCCGCCCTTACGTTACTGCG	1260
QY	1261	CGNAGCGCTTGGAAATAGCGCGGTGTGCTTATATATGTTTTCACCATATG	1320
DB	1261	CGNAGCGCTTGGAAATAGCGCGGTGTGCTTATATATGTTTTCACCATATG	1320
QY	1321	CCGCTTTTGGCAATGTGAGGCGCCCGAAACCTTGGCCCTGTCTTTCGAGAGCATTCCT	1380
DB	1321	CCGCTTTTGGCAATGTGAGGCGCCCGAAACCTTGGCCCTGTCTTTCGAGAGCATTCCT	1380
QY	1381	AGGGGTCTTTCCTCTCGCCTTTCGCAAGGAATGCAAGGTCTGTTGAATGTGGAAGGAGCA	1440
DB	1381	AGGGGTCTTTCCTCTCGCCTTTCGCAAGGAATGCAAGGTCTGTTGAATGTGGAAGGAGCA	1440
QY	1441	GTTTCTCTGGAGCTTCTTGAACACAAACCTTGTAGCGACCCCTTTCGACGAGCGG	1500
DB	1441	GTTTCTCTGGAGCTTCTTGAACACAAACCTTGTAGCGACCCCTTTCGACGAGCGG	1500
QY	1501	AACCCCGCACTCTGCGCACAGGTCTCTGCGGCAAAAGCCACGTGTATAGATACACCT	1560
DB	1501	AACCCCGCACTCTGCGCACAGGTCTCTGCGGCAAAAGCCACGTGTATAGATACACCT	1560
QY	1561	GCAAGCGGCAACACCCCGAGTGTGAGTTGAGTGTGGAAGAGTCAAA	1620
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DB	1681	ATGGGATCTGATCTGGGGCTCGGTGCACATGCTTTACATGTTTGTAGTGTGAGTTAAAA	1740
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Db 7982 AGATCAAGT 7989

RESULT 11

ABK91440

ID ABK91440 standard; DNA; 10690 BP.

XX

AC ABK91440;

XX

XX 15-NOV-2002 (first entry)

XX

XX Hepatitis C virus vector construct pHVNeo.17m7.

XX

XX HCV; ss; pHVNeo.17m2; adaptive mutation; liver failure; cirrhosis;

XX hepatocellular carcinoma; NS3; NS5; encephalomyocarditis virus; EMCV;

XX internal ribosome entry site; IRES; NS5A; HCV replication; mutant.

XX

OS Hepatitis C virus.

OS Encephalomyocarditis virus.

OS Escherichia coli.

OS Enterobacteria phage T7.

```
OS Synthetic.
XX Key Location/Qualifiers
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FT FT 342..1181
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FT CDS /*tag= d
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FT /*note= "Comprising NS3, NS4A, NS4B, NS5A and NS5B"
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FT /*tag= e
FT mutation replace(5243,C)
FT /*tag= f
FT 7759..7991
FT /*tag= g
FT 7992..10690
FT misc_feature /*tag= h
FT /*note= "Plasmid derived sequences"
XX WO200259321-A2.
XX 01-AUG-2002.
XX 16-JAN-2002; 2002WO-EF000526.
XX 23-JAN-2001; 2001US-0263479P.
XX (RICE-) IST RICERCHE BIOL MOLECOLARE ANGELETTI.
XX De Francesco R, Migliaccio G, Paonessa G;
XX WPI; 2002-599793/64.
XX New Hepatitis C virus (HCV) replicons comprising altered HCV NS3 or HCV
XX NS5 encoding region, or encephalomyocarditis virus (EMCV) internal
XX ribosome entry site (IRES) region, useful in studying HCV replication and
XX expression.
XX Claim 16; Page; 69pp; English.
XX The invention relates to nucleic acid molecules comprising altered HCV
XX NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV)
XX internal ribosome entry site (IRES) region coding for one or more NS3,
XX NS5A, or EMCV IRES mutations, respectively. The location of the mutations
XX are detailed in the specification. Also included are (1) an expression
XX vector comprising a nucleotide sequence coding for the altered nucleic
XX acids, which is transcriptionally coupled to an exogenous promoter; (2) a
XX recombinant cell human hepatoma cell comprising the altered nucleic acids
XX ; (3) a recombinant cell produced by introducing into a human hepatoma
XX cell the altered nucleic acids; (4) producing an HCV (hepatitis C virus)
XX replicon enhanced cell or which containing a functional HCV replicon; (5)
XX an HCV replicon enhanced cells made in the method; and (6) measuring the
XX ability of a compound to affect HCV activity. The HCV replicons and HCV
XX replicon enhanced cells are useful in studying HCV replication and
XX expression, and HCV and host cell interactions, producing HCV RNA and
XX proteins, and providing a system for measuring the ability of a compound
XX to modulate one or more HCV activities e.g. to discover drugs which may
XX treat HCV mediated diseases such as liver failure, cirrhosis and
XX hepatocellular carcinoma. The present sequence is an HCV based vector
XX pHCVNeo.17 mutant of the invention. Note: The present sequence is not
XX shown in the specification but was created by the indexer using the HCV
XX vector sequence appearing as ABK391412 and the information in Claim 16
XX
XX SQ Sequence 10690 BP; 2333 A; 3045 C; 2908 G; 2404 T; 0 U; 0 Other;
XX Query Match 99.9%; Score 7982.4; DB 6; Length 10690;
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 7986; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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QY 61 TCTTCACGACGAAAGCGTCTAGCCATGGCTTAGTATGATAGTGTCTGTGAGGCTTCCAGGAC 120
DB 61 TCTTCACGACGAAAGCGTCTAGCCATGGCTTAGTATGATAGTGTCTGTGAGGCTTCCAGGAC 120
QY 121 CCCCCTTCCCGGAGAGCCATAGTGGTCTGCGGAAACCGGTGAGTACACCGGAATTCGCCAG 180
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DB 361 CTCGAAGAAACCAAGGCGCGCATGATTTGAACAAGATGATTTGACGCGAGTTCTC 420
QY 421 CGGCGCTTTGGGTGGAGAGGCTATTTCGGCTATGACTGGGCACAAACAGCAATCGGTGCT 480
DB 421 CGGCGCTTTGGGTGGAGAGGCTATTTCGGCTATGACTGGGCACAAACAGCAATCGGTGCT 480
QY 481 CTGATGCCCGCTGTTCCGGCTGTGAGCGAGGGCGCGCGGTCTTTTGTCAAGACCG 540
DB 481 CTGATGCCCGCTGTTCCGGCTGTGAGCGAGGGCGCGCGGTCTTTTGTCAAGACCG 540
QY 541 ACTGTCCGGTCCCTGAAATGACTGACGACGAGGCGCGGTCTATCGTGGCTGGCCA 600
DB 541 ACTGTCCGGTCCCTGAAATGAACTGACGACGAGGCGCGGTCTATCGTGGCTGGCCA 600
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DB 601 CGACGGCGCTTCTTCCGCGAGTGTCTGACGCTTGTCTGAAAGCGGAGGAGCTGGC 660
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DB 721 AAGTATCCATCATGGCTGATGCAATGCGGCGGTGATAGCTTGTATCCGGCTACCTGCC 780
QY 781 CATTCGACCAACCAAGCGAAACATCGCATCGAGCGAGCAGCTACTCGGATGGAAGCGGTC 840
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DB 841 TTGTCGATCAGGATGATCTGGAGGAAGAGATCAGGGGCTCGGCCAGCGAAGCTGTTCG 900
QY 901 CCAGGCTCAAGGCGCGCATGCCCGAGAGATCTGTCGTGACCGATCGGATGCGATGCGCT 960
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Qy 1201 GTTTCCTCTAGCGGATCAATTCGCGCTTCTCGCTCCCTCCCTCCCTCCCTCCCTCCCT 1260
Db 1201 GTTTCCTCTAGCGGATCAATTCGCGCTTCTCGCTCCCTCCCTCCCTCCCTCCCTCCCT 1260
Qy 1261 CGAAGCCCTTGGAAATAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
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Qy 1381 AGGGTCTTTCCCTCTCGCCAAAGGAATGCAAGGTCTGTTGAATGCTGCTGAAGGAACA 1440
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Qy 1501 AACCCCTTGGCGACAGGTGCTCTGCGGCGCAAAAGCCACGCTGTAAGATACACCT 1560
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Qy 1681 ATGGGATCTGATCTGGGCTCTGGTGACATGCTTTACATGCTTTAGTTCGAGGTAAAA 1740
Db 1681 ATGGGATCTGATCTGGGCTCTGGTGACATGCTTTACATGCTTTAGTTCGAGGTAAAA 1740
Qy 1741 AACGTCTAGGCCCCCGGAAACAGCGGACGTTGTTTCCCTTTGAAACACGATAATACC 1800
Db 1741 AACGTCTAGGCCCCCGGAAACAGCGGACGTTGTTTCCCTTTGAAACACGATAATACC 1800
Qy 1801 ATGGCGCTATTACGGCTACTCCCAAGACGAGCGGCTACTTGGCTGCATCATCACT 1860
Db 1801 ATGGCGCTATTACGGCTACTCCCAAGACGAGCGGCTACTTGGCTGCATCATCACT 1860
Qy 1861 AGCCTCACAGCCCGGACAGAAACAGGTCCAGGGGAGGTCCAGGTGCTTCCACCGCA 1920
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Qy 1921 ACACATCTTTCTGGCGACTGCTGCTCAATGGCGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1980
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Qy 1981 GGCTCAAGACCTTTCGGCGGCAAGGCGGCTTCCCTTGAACCATGACCATGCTGC 2040
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Qy 2161 GCGGACAGCAGGGGAGCCTACTCTCCCGCAGGCCGCTCTCTACTTGAAGGGCTCTTGG 2220
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Qy 2221 GCGGTCCACTGCTCTGCGCCCTCGGGGACGCTGTGGGCACTTTTCGGGCTGCCGTGTC 2280
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Qy 3181 CAGCGCGAGGACGCTGCTAGGGGAGGATGGGCAATTTACAGGTTTGTGACTCCAGGA 3240
Db 3181 CAGCGCGAGGACGCTGCTAGGGGAGGATGGGCAATTTACAGGTTTGTGACTCCAGGA 3240

QY	3241	GAACGGCCCTCGGGCATGTTGGATTCCTCGGTTCTGTGCGAGTGTCTATGACGCGGCTGT	3300	Db	4321	TTTAAAGTCAATGAGCGGCGAGATGCCCTCCACCGAGGACCTGGTTAAACCTACTCCCTGCT	4380
Db	3241	GAACGGCCCTCGGGCATGTTGGATTCCTCGGTTCTGTGCGAGTGTCTATGACGCGGCTGT	3300	QY	4381	ATCCCTCTCCCTTGGCGCCCTAGTCTCGGGGTCTGTGCGAGCGATCTACTCGTGGCAC	4440
QY	3301	GCTTGGTACAGCTCACGCCGCCCGAGACCTCAGTTAGGTTGCGGCTTACCTAAACACA	3360	Db	4381	ATCCCTCTCCCTTGGCGCCCTAGTCTCGGGGTCTGTGCGAGCGATCTACTCGTGGCAC	4440
Db	3301	GCTTGGTACAGCTCACGCCGCCCGAGACCTCAGTTAGGTTGCGGCTTACCTAAACACA	3360	QY	4441	GTGGGCCAGAGGGGCTGTGAGTGAGTAAACCGGCTGATAGCGTTCCGCTTCGCGG	4500
QY	3361	CCAGGGTTCCCGTCTGCGAGACCAATCTGGAGTTCTGGAGAGCGTCTTTACAGGCTC	3420	Db	4441	GTGGGCCAGAGGGGCTGTGAGTGAGTAAACCGGCTGATAGCGTTCCGCTTCGCGG	4500
Db	3361	CCAGGGTTCCCGTCTGCGAGACCAATCTGGAGTTCTGGAGAGCGTCTTTACAGGCTC	3420	QY	4501	GCTAAACCAAGTCTCCCGACCTATGTCCTGAGAGGACGCTGACGACGTTGCTCACT	4560
QY	3421	ACCCATAGACGCCATTTCTGTCACAGATTAAGCAGGAGAGCAACTTCCCTAC	3480	Db	4501	GCTAAACCAAGTCTCCCGACCTATGTCCTGAGAGGACGCTGACGACGTTGCTCACT	4560
Db	3421	ACCCATAGACGCCATTTCTGTCACAGATTAAGCAGGAGAGCAACTTCCCTAC	3480	QY	4561	CAGATCTCTCTAGTCTTACCATCTACTAGCTGCTGAAGAGGCTTCCACAGTGATCAAC	4620
QY	3481	CTGGTAGCATACAGGCTACGGTGTGCGCCAGGGCTCAGGCTCCACTCCATCGTGGAC	3540	Db	4561	CAGATCTCTCTAGTCTTACCATCTACTAGCTGCTGAAGAGGCTTCCACAGTGATCAAC	4620
Db	3481	CTGGTAGCATACAGGCTACGGTGTGCGCCAGGGCTCAGGCTCCACTCCATCGTGGAC	3540	QY	4621	GAGGACTGTCTCCACGCCATGCTCCGGCTCGTGCTAAAGATGTTTGGGATTGGATATGC	4680
QY	3541	CAAAATGTGAAGTGTCTATACGGCTAAAGCCCTACGCTGCACGGGCCAAACGCCCCCTG	3600	Db	4621	GAGGACTGTCTCCACGCCATGCTCCGGCTCGTGCTAAAGATGTTTGGGATTGGATATGC	4680
Db	3541	CAAAATGTGAAGTGTCTATACGGCTAAAGCCCTACGCTGCACGGGCCAAACGCCCCCTG	3600	QY	4681	ACGGTGTGACTGATTTCAAGACCTGGCTCCAGTCCAAGCTCCTGCGCGGATTGCGCGGA	4740
QY	3601	TATAGCTGGAGCCGTTCAAAACAGAGTTACTTACACACACCCCATAAATACATC	3660	Db	4681	ACGGTGTGACTGATTTCAAGACCTGGCTCCAGTCCAAGCTCCTGCGCGGATTGCGCGGA	4740
Db	3601	TATAGCTGGAGCCGTTCAAAACAGAGTTACTTACACACACCCCATAAATACATC	3660	QY	4741	GTCCCTCTCTCTAGTCAAGCTGCTGAGGAGTCTGCGGGGCGACGCGATCATG	4800
QY	3661	ATGGCATGATGTGCGCTGACCTGGAGTCTGTCACGAGCACCTGGTGTGGTGGCAGG	3720	Db	4741	GTCCCTCTCTCTAGTCAAGCTGCTGAGGAGTCTGCGGGGCGACGCGATCATG	4800
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QY	3721	GTCTAGAGCTGTGCGCGGTATTCCTGACAAACAGGAGTCTGTCATTTACCGGAGTTC	3780	Db	4801	CAAAACCACTGCCATGTGGAGCACACGATCACCGACATGTGAAAACCGGTTCCATGAGG	4860
Db	3721	GTCTAGAGCTGTGCGCGGTATTCCTGACAAACAGGAGTCTGTCATTTACCGGAGTTC	3780	QY	4861	ATCGTGGGCTTAGGACCTGTAGTAAACGCTGATGGAACATTTCCCATTAACGCGTAC	4920
QY	3781	ATCATCTGTGCGGAAGCGGCGCATCTTCCCGACAGGAGTCTTACCGGAGTTC	3840	Db	4861	ATCGTGGGCTTAGGACCTGTAGTAAACGCTGATGGAACATTTCCCATTAACGCGTAC	4920
Db	3781	ATCATCTGTGCGGAAGCGGCGCATCTTCCCGACAGGAGTCTTACCGGAGTTC	3840	QY	4921	ACACGGGCGCTTGCACGCGCTTCCCGGCGCCAAATTTCTAGGGGCTGTGCGGGTG	4980
QY	3841	GATGAGATGAAGTGCCTCACACCTCCCTTATACGAAACAGGAAATGACGCTCGCC	3900	Db	4921	ACACGGGCGCTTGCACGCGCTTCCCGGCGCCAAATTTCTAGGGGCTGTGCGGGTG	4980
Db	3841	GATGAGATGAAGTGCCTCACACCTCCCTTATACGAAACAGGAAATGACGCTCGCC	3900	QY	4981	GCTGCTGAGAGTACCTGAGGTTACGCGGTTGGGGATTTCCACTACGTCAGCGGATG	5040
QY	3901	GAACAAATCAACAGAGGATCGGCTTGCACACAGCCCTTCCCTTACGAAACAGGAAATG	3960	Db	4981	GCTGCTGAGAGTACCTGAGGTTACGCGGTTGGGGATTTCCACTACGTCAGCGGATG	5040
Db	3901	GAACAAATCAACAGAGGATCGGCTTGCACACAGCCCTTCCCTTACGAAACAGGAAATG	3960	QY	5041	ACCACCTGACAAACGTAAGTGCCTGTACAGTTCCGGGCGCCCGAAATTTCTTCAAGAGTG	5100
QY	3961	GCTGCTCCGCTGGAATCCAAAGTGGGAGCTTCCGAGCCCTTCCGCGGAAAGCATATG	4020	Db	5041	ACCACCTGACAAACGTAAGTGCCTGTACAGTTCCGGGCGCCCGAAATTTCTTCAAGAGTG	5100
Db	3961	GCTGCTCCGCTGGAATCCAAAGTGGGAGCTTCCGAGCCCTTCCGCGGAAAGCATATG	4020	QY	5101	GATGGGCTGGGTTGCACAGGTACGCTCCAGCGTGCAAAACCCCTCTACGCGGAGGAGTC	5160
QY	4021	TGGAATTTTATACGCGGATACAAATTTTAGAGGCTTGTCCACTCTGCTGCGGAAACCC	4080	Db	5101	GATGGGCTGGGTTGCACAGGTACGCTCCAGCGTGCAAAACCCCTCTACGCGGAGGAGTC	5160
Db	4021	TGGAATTTTATACGCGGATACAAATTTTAGAGGCTTGTCCACTCTGCTGCGGAAACCC	4080	QY	5161	ACATTCCTGCTCGGGCTCAATCAATACCTGTTGGGTCAAGCTCCATCGAGCGCGGAA	5220
QY	4081	GCGATAGCATCTGATGGAATTCAGAGTGGCGGCTTCCAGAGCTTCTGGGCGAAGCATATG	4140	Db	5161	ACATTCCTGCTCGGGCTCAATCAATACCTGTTGGGTCAAGCTCCATCGAGCGCGGAA	5220
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QY	4141	ACCTCTCTGTTTAAACATCTGCGGGGATGGTGGCGGCTTGTCCACTCTGCTCCAGCGCT	4200	Db	5221	CCGGAAGTGGCTTGCACAGGTACGCTCCAGCGTCCACCGCTCCACATTAACGCGGAGACG	5280
Db	4141	ACCTCTCTGTTTAAACATCTGCGGGGATGGTGGCGGCTTGTCCACTCTGCTCCAGCGCT	4200	QY	5281	GCTAAGCGTGGCTTGCACAGGTACGCTCCAGCGTCCACCGCTCCACATTAACGCGGAGACG	5340
QY	4201	GCTTCTGCTTGTAGGCGCGGATCGCTGAGAGCGGCTTGTGGCAGCATAGGCTTGGG	4260	Db	5281	GCTAAGCGTGGCTTGCACAGGTACGCTCCAGCGTCCACCGCTCCACATTAACGCGGAGACG	5340
Db	4201	GCTTCTGCTTGTAGGCGCGGATCGCTGAGAGCGGCTTGTGGCAGCATAGGCTTGGG	4260	QY	5341	CTGCTGCGCTTCTTTGAAGGCAACATGCACTACCGCTCATGCTCCCGGAGCGTGC	5400
QY	4261	AAGGTGCTTGTGATATTTTGGCAGGTTATGGAGCAGGCTTGGCAGCGGCTCGTGCC	4320	Db	5341	CTGCTGCGCTTCTTTGAAGGCAACATGCACTACCGCTCATGCTCCCGGAGCGTGC	5400
Db	4261	AAGGTGCTTGTGATATTTTGGCAGGTTATGGAGCAGGCTTGGCAGCGGCTCGTGCC	4320	QY	5401	CTCATCGAGCGCAACCTCTGTCGCGAGAGATGGCGGGAACATCAACCGGCTGGAG	5460
QY	4321	TTTAAAGTCAATGAGCGGCGAGATGCCCTCCACCGAGGACCTGGCTAAACCTACTCCCTGCT	4380				

QY 7621 TTATCCAGCTGTTGCTGCTGTTTACAGCGGGGAGACATATATCAGAGCTGCTGCT 7680
DB |||||||
QY 7621 TTATCCAGCTGTTGCTGCTGTTTACAGCGGGGAGACATATATCAGAGCTGCTGCT 7680
DB |||||||
QY 7681 GCCCGACCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 7740
DB |||||||
QY 7681 GCCCGACCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 7740
DB |||||||
QY 7741 CTACTCCCAACCGATGAGAAAGCGGAGCTAAACACTCCAGGCCCAATAGGCCATCCGTTT 7800
DB |||||||
QY 7741 CTACTCCCAACCGATGAGAAAGCGGAGCTAAACACTCCAGGCCCAATAGGCCATCCGTTT 7800
DB |||||||
QY 7801 TTTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7860
DB |||||||
QY 7801 TTTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7860
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DB |||||||
QY 7921 TAGCTGTGAAGGTCGCTGAGCGCTTGACTGTCAGAGAGTGTGATGCTGCTCTGTC 7980
DB |||||||
QY 7921 TAGCTGTGAAGGTCGCTGAGCGCTTGACTGTCAGAGAGTGTGATGCTGCTCTGTC 7980
DB |||||||
QY 7981 AGATCAAGTACT 7992
DB |||||||
QY 7981 AGATCAAGTACT 7992
DB |||||||

RESULT 12

AAD25322 standard; cDNA; 7989 BP.

XX AAD25322;

XX 12-MAR-2002 (first entry)

XX Hepatitis C virus (HCV) replBartMan/Avail cDNA.

XX Hepatitis C virus; HCV; transfection; infection; virus neutralisation;

XX gene therapy; vaccine; immunoprotection; hepatotropic; virucide; liver;

XX ss.

XX Hepatitis C virus.

XX Key Location/Qualifiers

XX CDS 1801..7758

XX /*tag= a

XX /product= "HCVreplBartMan polypeptide"

XX 7766

XX /*tag= b

XX /note= "Nucleotide creating Avail site"

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The invention relates to Hepatitis C virus (HCV) variants which include polynucleotides comprising non-naturally occurring HCV sequence and HCV variants that have a transfection efficiency and ability to survive subpassage greater than HCV that have wild-type polypeptide coding regions. The polynucleotides of the invention are useful for identifying a cell line that is permissive for infection with HCV and detecting replication of HCV in cells of the cell line. They are also useful for testing a compound for anti-viral properties and for inhibiting HCV infection. They are also useful for the generation of defined HCV virus stocks to develop in vitro and in vivo assays for virus neutralisation, attachment, penetration and entry, structure/function studies on HCV proteins and RNA elements and identification of new antiviral targets, a systematic survey of cell culture systems and conditions to identify those that support wild-type and variant HCV RNA replication and particle release, production of adaptive HCV variants capable of more efficiency replication in cell culture, production of HCV variants with altered tissue or species tropism, establishment of alternative animal models for inhibitor evaluation including those supporting HCV variant replication, development of cell-free HCV replication assays, production of immunogenic HCV particles for vaccination, engineering of attenuated HCV derivatives as possible vaccine candidates, engineering of attenuated or defective HCV derivatives for expression of heterologous gene products for gene therapy and vaccine applications and for utilisation of the HCV glycoproteins for targeted delivery of therapeutic agents to the liver or other cell types with appropriate receptors. Vaccine comprising these sequences is useful for inducing immunoprotection to HCV in a primate. The present sequence is Hepatitis C virus (HCV) replBartMan/Avail cDNA

XX SQ Sequence 7989 BP; 1647 A; 2369 C; 2242 G; 1731 T; 0 U; 0 Other;

Query Match 99.9%; Score 7981; DB 6; Length 7989;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 7984; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 GCCAGCCCCCGATTGGGGCGGACACTCCACCATAGATCACTCCCTGTGAGGAACTACTG 60
DB 1 GCCAGCCCCCGATTGGGGCGGACACTCCACCATAGATCACTCCCTGTGAGGAACTACTG 60
QY 61 TCTTACCGCAGAAAGCGTCTAGCCATGGGTTAGTATGATGCTGTCGTCAGACCTCCAGGAC 120
DB 61 TCTTACCGCAGAAAGCGTCTAGCCATGGGTTAGTATGATGCTGTCGTCAGACCTCCAGGAC 120
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DB 121 CCCCCCTCCCGGAGAGCCATAGTGTCTCGGAAACCGGTGAGTACACCGGAATCCGAG 180
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DB 301 GTGCTTTCGAGTGTCCCGGGAGGTCTCGTAGACCGGTGACACCGATGAGCAAACTAAAC 360
QY 361 CTCAAAGAAAACCAAGGGCGCCATGATTTGAAACAAGATGATTTGCAAGGTTCTC 420
DB 361 CTCAAAGAAAACCAAGGGCGCCATGATTTGAAACAAGATGATTTGCAAGGTTCTC 420
QY 421 CGGCCGCTTGGGTGAGAGGCTATTTCGGCTATGCTGGGCAACAGACAATCGGCTGCT 480
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QY 541 ACCTGTCCGGTCCCTGMAATGAATCAGGACGAGCGCGCTATCGTGGCTGGCCA 600
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Db 721 AAGTATCCATCATGCTGANTGAAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCC 780
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QY 5941 TCTACCGTAAGCGAGGAGGCTAGTAGGACGCTGTCTGTCTCGATGCTCTACACATGG 6000
Db 5941 TCTACCGTAAGCGAGGAGGCTAGTAGGACGCTGTCTGTCTCGATGCTCTACACATGG 6000
QY 6001 ACAGGCGCCCTGATCACGCCATGCGCTGGGAGGAAACCAAGCTGCCATCAATGCACTG 6060
Db 6001 ACAGGCGCCCTGATCACGCCATGCGCTGGGAGGAAACCAAGCTGCCATCAATGCACTG 6060
QY 6061 AGCAACTCTTTGCTCCGTCACCAACTTTGCTATGTATGCTACAACTCTGCGAGCCGACG 6120
Db 6061 AGCAACTCTTTGCTCCGTCACCAACTTTGCTATGTATGCTACAACTCTGCGAGCGAAGC 6120
QY 6121 CTGGGCGAGAAAGGTCACTTTGACAGACTGCGAGTCTCTGGACGACCACTTACCGGGAC 6180
Db 6121 CTGGGCGAGAAAGGTCACTTTGACAGACTGCGAGTCTCTGGACGACCACTTACCGGGAC 6180
QY 6181 GTGCTCAAGGAGATGAAGCGAAGCGTCCACAGTAAAGGCTAAACTTCTATCCGTGGAG 6240
Db 6181 GTGCTCAAGGAGATGAAGCGAAGCGTCCACAGTAAAGGCTAAACTTCTATCCGTGGAG 6240
QY 6241 GAAGCTCTAAGCTGACGCGCCCACTTCGCGCCAGATCTAAATTTGGCTATGGGCAAG 6300
Db 6241 GAAGCTCTAAGCTGACGCGCCCACTTCGCGCCAGATCTAAATTTGGCTATGGGCAAG 6300
QY 6301 GACGTCCGGAACCTTATCCAGCAAGCGCTTAAACCACTCCGCTCGGTGGAAGACTTG 6360
Db 6301 GACGTCCGGAACCTTATCCAGCAAGCGCTTAAACCACTCCGCTCGGTGGAAGACTTG 6360
QY 6361 CTGGAAGACTGAGACCACTTGAACCACTTGAACCACTTGAACCACTTGAACCACTTGAAC 6420
Db 6361 CTGGAAGACTGAGACCACTTGAACCACTTGAACCACTTGAACCACTTGAACCACTTGAAC 6420
QY 6421 GTCCAAACAGAGAGGCGCGCAAGCGCTGCTGCTTATCGCTTATCCAGATTTGGG 6480
Db 6421 GTCCAAACAGAGAGGCGCGCAAGCGCTGCTGCTTATCGCTTATCCAGATTTGGG 6480
QY 6481 GTTCGTGTGCGAGAAATGGCCCTTTACGATGTGTCTCCACCTCCCTCAGGCGCTG 6540
Db 6481 GTTCGTGTGCGAGAAATGGCCCTTTACGATGTGTCTCCACCTCCCTCAGGCGCTG 6540
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Db 6601 GCCTGGAAGCGAAGAAATGCGCTTATGCGCTTATGCAATATGACCCCGCTGTTGACTCA 6660
QY 6661 ACGTCTCAGAGATGACATCCGTTGAGGAGTCAATCTACCAATGTTGACTTGGCC 6720
Db 6661 ACGTCTCAGAGATGACATCCGTTGAGGAGTCAATCTACCAATGTTGACTTGGCC 6720
QY 6721 CCCGAGCCGACAGGCGATTAAGTCTGCTCAGAGGCGCTTACATCGGGGGCGCCCTG 6780
Db 6721 CCCGAGCCGACAGGCGATTAAGTCTGCTCAGAGGCGCTTACATCGGGGGCGCCCTG 6780
QY 6781 ACTAATTTCTAAGGCGAAGAAATGCGCTTATGCGCGGTGCGCGAGCGGTGACTGACG 6840
Db 6781 ACTAATTTCTAAGGCGAAGAAATGCGCTTATGCGCGGTGCGCGAGCGGTGACTGACG 6840
QY 6841 ACCAGCTGCGGTAAATACCTTCAATGTTACTTGAAGCGCGCTGCGGCTGTGAGCTGCG 6900
Db 6841 ACCAGCTGCGGTAAATACCTTCAATGTTACTTGAAGCGCGCTGCGGCTGTGAGCTGCG 6900
QY 6901 AAGCTCCAGACTGCGAGTCTCGTATGCGGAGACGACCTTGTCTGTTACTGTGAAAGC 6960
Db 6901 AAGCTCCAGACTGCGAGTCTCGTATGCGGAGACGACCTTGTCTGTTACTGTGAAAGC 6960
QY 6961 GCGGGGACCCAGAGGAGCGGAGCGCTTACGCGGCTTACCGGAGGCTATGACTAGATAC 7020
Db 6961 GCGGGGACCCAGAGGAGCGGAGCGCTTACGCGGCTTACCGGAGGCTATGACTAGATAC 7020

QY	7021	TCTGCCCCCTGGGACCGCCCAACAGAAATACGACTTGGAGTTGATAACATCATGC	7080
Db	7021	TCTGCCCCCTGGGACCGCCCAACAGAAATACGACTTGGAGTTGATAACATCATGC	7080
QY	7081	TCCTCCAAATGTGTACGTGGGACAGATGATCTGGCCAAAAGGGTGTACTATCTCACCCGT	7140
Db	7081	TCCTCCAAATGTGTACGTGGGACAGATGATCTGGCCAAAAGGGTGTACTATCTCACCCGT	7140
QY	7141	GACCCACCAACCCCTTGTGCGGGGTGGTGGGAGACAGCTAGACACACTCCAGTCAAT	7200
Db	7141	GACCCACCAACCCCTTGTGCGGGGTGGTGGGAGACAGCTAGACACACTCCAGTCAAT	7200
QY	7201	TCCTGGCTAGGGAACATCATATGATGCGCCCAACTTGTGGCCAGGATGATCCCTGATG	7260
Db	7201	TCCTGGCTAGGGAACATCATATGATGCGCCCAACTTGTGGCCAGGATGATCCCTGATG	7260
QY	7261	ACTCATTTCTTCTCCATCCTTCTAGCTTCAGGAAACAATTGAAAAAGCCCTAGATTTCTCAG	7320
Db	7261	ACTCATTTCTTCTCCATCCTTCTAGCTTCAGGAAACAATTGAAAAAGCCCTAGATTTCTCAG	7320
QY	7321	ATCTACGGGCGCTGTATCTCCATAGGCCACTTGAACCTCAGATCATTTCAACGACTC	7380
Db	7321	ATCTACGGGCGCTGTATCTCCATAGGCCACTTGAACCTCAGATCATTTCAACGACTC	7380
QY	7381	CATGGCCTTAGCGCATTTTCACTCCATAGTTACTCTCCAGGTGAGATCAATAGGTTGGCT	7440
Db	7381	CATGGCCTTAGCGCATTTTCACTCCATAGTTACTCTCCAGGTGAGATCAATAGGTTGGCT	7440
QY	7441	TCATGCCCTCAGGAAACTTGGGGTACCGCCCTTGCAGTCTGGAGACATCGGGCCAGAAGT	7500
Db	7441	TCATGCCCTCAGGAAACTTGGGGTACCGCCCTTGCAGTCTGGAGACATCGGGCCAGAAGT	7500
QY	7501	GTCGCGCTTAGCTACTGTCCAGGGGGGAGGGCTGCCACTTGTGGCAAGTACCTCTTC	7560
Db	7501	GTCGCGCTTAGCTACTGTCCAGGGGGGAGGGCTGCCACTTGTGGCAAGTACCTCTTC	7560
QY	7561	AACCTGGCGAGTAAGGACCAAGCTCAAACTCACTCCAATCCCGGCTGGCTGCCAGTACCTTTC	7620
Db	7561	AACCTGGCGAGTAAGGACCAAGCTCAAACTCACTCCAATCCCGGCTGGCTGCCAGTACCTTTC	7620
QY	7621	TTATCCAGCTGGTTTGGTTGCTGGTTACAGCGGGGGAGACATATATCAAGCTGTCTCGT	7680
Db	7621	TTATCCAGCTGGTTTGGTTGCTGGTTACAGCGGGGGAGACATATATCAAGCTGTCTCGT	7680
QY	7681	GCCGACCCCGCTGTTTCATGTGTGCTACTCCTACTTCTGTAGGGGTAGGCATCTAT	7740
Db	7681	GCCGACCCCGCTGTTTCATGTGTGCTACTCCTACTTCTGTAGGGGTAGGCATCTAT	7740
QY	7741	CTACTCCCCAACCGATGAACGGGAGTAAACACTCCAGGCGAATAGGCCATCTCTGTTT	7800
Db	7741	CTACTCCCCAACCGATGAACGGGAGTAAACACTCCAGGCGAATAGGCCATCTCTGTTT	7800
QY	7801	TTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	7860
Db	7801	TTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	7860
QY	7861	TTTTTTCCTCTTTTCTTTTCTTTTCTTTTGGTCTCCATCTTAGCCCTAGTCAAGGC	7920
Db	7861	TTTTTTCCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTGGTCTCCATCTTAGCCCTAGTCAAGGC	7920
QY	7921	TAGCTGTGAAGAGTCCGTGAGCCGCTGACGTGACAGAGTCTCTATAGTGGCCTCTCTGC	7980
Db	7921	TAGCTGTGAAGAGTCCGTGAGCCGCTGACGTGACAGAGTCTCTATAGTGGCCTCTCTGC	7980
QY	7981	AGATCAAGTACT 7992	
Db	7981	AGATCAAGTACT 7992	

RESULT 14

AA147277

ID AA147277 standard; DNA: 7992 BP.

QY 301 GTGCTGCGAGTCCCCGGGAGGTCTCTGTAGACCGGTGACACCATGAGCAGCAATCCTAAAC 360
DB 301 GTGCTTGCGAGTGCCCCGGGAGGTCTCTGTAGACCGGTGACACCATGAGCAGCAATCCTAAAC 360
QY 361 CTCAAAGAAAACCAAGGGCGGCGCATGATTGAACAAGATGGATGCAACGAGTTCTC 420
DB 361 CTCAAAGAAAACCAAGGGCGGCGCATGATTGAACAAGATGGATGCAACGAGTTCTC 420
QY 421 CGGCGCGTGGGTGGAGAGGCTATTGCGCTATGACTGGGCAACAAGCAAAATCGGCTGCT 480
DB 421 CGGCGCGTGGGTGGAGAGGCTATTGCGCTATGACTGGGCAACAAGCAAAATCGGCTGCT 480
QY 481 CTGATGCCCGCGTGTTCGGGCTGTGAGCGCAGGGCGCCCGGTCTCTTTTGTCAAGACCG 540
DB 481 CTGATGCCCGCGTGTTCGGGCTGTGAGCGCAGGGCGCCCGGTCTCTTTTGTCAAGACCG 540
QY 541 ACCTGTCCGGTGCCTGATGAACTGCGAGGAGCGAGCGCGGCTATGCTGGCTGGGCA 600
DB 541 ACCTGTCCGGTGCCTGATGAACTGCGAGGAGCGAGCGCGGCTATGCTGGCTGGGCA 600
QY 601 CGAACGGCGTCTCTTGGCGAGCTGTGCTCGAGTGTGCTCACTGAAGCGGGAAGGACTGCG 660
DB 601 CGAACGGCGTCTCTTGGCGAGCTGTGCTCGAGTGTGCTCACTGAAGCGGGAAGGACTGCG 660
QY 661 TGCTATTGGGGAAGTCCGGGCGAGGATCTCTGCTCATCTCACCTTGCTCTGCGCGAGA 720
DB 661 TGCTATTGGGGAAGTCCGGGCGAGGATCTCTGCTCATCTCACCTTGCTCTGCGCGAGA 720
QY 721 AAGTATCCATCATGCTGATGCAATGCGGCGGCTGCATACGCTTGTATCCGCTACCTGCC 780
DB 721 AAGTATCCATCATGCTGATGCAATGCGGCGGCTGCATACGCTTGTATCCGCTACCTGCC 780
QY 781 CATTCGACACCAACCGGAAAATCGCATCGAGCGAGCAGTACTCGGATGGAAGCGGTC 840
DB 781 CATTCGACACCAACCGGAAAATCGCATCGAGCGAGCAGTACTCGGATGGAAGCGGTC 840
QY 841 TTGTGATCAGATGATCTGACGAGAGATCAGGGGCTCGCGCAGCCGAACCTGTTTCG 900
DB 841 TTGTGATCAGATGATCTGACGAGAGATCAGGGGCTCGCGCAGCCGAACCTGTTTCG 900
QY 901 CCAGGCTCAAGCGCGGATGCCGAGCGGAGGATCTCGTGTGACCCCATGCGGATGCT 960
DB 901 CCAGGCTCAAGCGCGGATGCCGAGCGGAGGATCTCGTGTGACCCCATGCGGATGCT 960
QY 961 GCTTGGCGAATATCATGTTGAAATGSCCGCTTTCTGGAATTCATCGACTGCGCGGC 1020
DB 961 GCTTGGCGAATATCATGTTGAAATGSCCGCTTTCTGGAATTCATCGACTGCGCGGC 1020
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DB 1021 TGGGTGTGGCGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTCCTGAAGAGC 1080
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DB 1081 TTGCGCGGATGAGCTGACCGCTTCTGCTGCTTTACGGTATCGCGCTCCCGATTGCG 1140
QY 1141 AGCGCATCGCTTCTATCGCTTCTTGACGAGTCTTCTGAGTTTAAACAGACCACAAG 1200
DB 1141 AGCGCATCGCTTCTATCGCTTCTTGACGAGTCTTCTGAGTTTAAACAGACCACAAG 1200
QY 1201 GTTTCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCTTAAGCTTACTGCG 1260
DB 1201 GTTTCCTCTAGCGGATCAATTCGCGCCCTCTACCTCCCGCCCTTAAGCTTACTGCG 1260
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DB 1261 CGAAGCGCTTGAATAGGCGGCTGCGTTGCTATATGTTATTTTCCACCATATG 1320
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DB 1321 CCGTCTTTTGGCAATGTAGGGCGCGGAAACCTGCGCTGTCTTGTGAGGAGCAATTCCT 1380
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DB 1381 AGGGGTCTTTCCTCTCGCCAAAGGAATGCAAGGTCTGTTGAATGTCGTAAGGAAGCA 1440
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DB 1441 GTTCTCTGGAAGCTTCTTGAAGACAAAACAGTCTGTAGCGACCTTTTGCAAGGACGCG 1500
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DB 1501 AACCCCGCCTGCGGACAGGTCCTCTGCGGCCAAAAGCCACGTTGTAAGATACACT 1560
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DB 1561 GCAAAAGGCGGACAAACCCAGTGCACGTTGTGAGTGTGATAGTGTGGAAGAAGTCAAA 1620
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DB 1621 TGGCTCTCTCAAGCGTATTCAACAAGGGGCTGGAAGGATGCCAGAGGTACCCCATTTG 1680
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DB 1681 ATGGGATCTGATCTGCGGCTCTGCGTGCACATGCTTTACATGTTTACTCGAGGTTAAAA 1740
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DB 1741 AACGCTAGGCGCCCGGAAACCAACCGGAGCGTGTTCCTTTGAAAACACGATATACC 1800
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QY 1861 AGCCTCACAGGCGGACAGGAAACAGGTCGAGGGGAGGTCAGGTCCTCCACCGCA 1920
DB 1861 AGCCTCACAGGCGGACAGGAAACAGGTCGAGGGGAGGTCAGGTCCTCCACCGCA 1920
QY 1921 ACACATCTTTCTTGGGACCTGCTCAATGCGCTGTGTTGGAAGTCTATCATGTTGCC 1980
DB 1921 ACACATCTTTCTTGGGACCTGCTCAATGCGCTGTGTTGGAAGTCTATCATGTTGCC 1980
QY 1981 GGCTCAAGAGACCTTGGCGGCCCAAGGGCCCAATCAACCAATGTACACCAATGTGGAC 2040
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DB 2041 CAGAACCTGCTGCGTGGCAAGCGCCCGGCGGCTTCTTGAACCATGACCTGTC 2100
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DB 2101 GGCAGCTCGGACCTTTACTTGGTCACGAGGATCGCGATGTCATTCGCTGCGCGCGG 2160
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Db 6841 ACCAGTCGGTAATACCTCACATGTTACTTTGAAGCGCTGCGGCTGTGAGCTGG 6900
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 Qy 7381 CATGGCTTATGCGCATTTTCACTCCATGATTTCTTCTTCTTCTTCTTCTTCTTCTTCT 7440
 Db 7381 CATGGCTTATGCGCATTTTCACTCCATGATTTCTTCTTCTTCTTCTTCTTCTTCTTCT 7440
 Qy 7441 TCAATGCTCAGGAACTTGGGGTACCGCTTGGAGTCTGGAGACATCGGCGCAGAGT 7500
 Db 7441 TCAATGCTCAGGAACTTGGGGTACCGCTTGGAGTCTGGAGACATCGGCGCAGAGT 7500
 Qy 7501 GTCCGCTAGGCTTGTCTTCCAGGGGAGGCTTCCACTTGTGCAAGTACCTTCTTCT 7560
 Db 7501 GTCCGCTAGGCTTGTCTTCCAGGGGAGGCTTCCACTTGTGCAAGTACCTTCTTCT 7560
 Qy 7561 AACTGGGAGTAAAGGACCAAGCTCAACTCACTCCATCCCGGCTGCTGCCAGTTGGAT 7620
 Db 7561 AACTGGGAGTAAAGGACCAAGCTCAACTCACTCCATCCCGGCTGCTGCCAGTTGGAT 7620
 Qy 7621 TTATCCAGCTGGTGTGCTTGTGTTACAGGGGGAGACATATACAGCCTGTCTCGT 7680
 Db 7621 TTATCCAGCTGGTGTGCTTGTGTTACAGGGGGAGACATATATACAGCCTGTCTCGT 7680
 Qy 7681 GCGGACCCCGCTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 7740
 Db 7681 GCGGACCCCGCTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 7740
 Qy 7741 CTACTCCCCAACCGATGAACGGGAGTAAACACTCCAGGCAATAGGCAATCTGTTTT 7800
 Db 7741 CTACTCCCCAACCGATGAACGGGAGTAAACACTCCAGGCAATAGGCAATCTGTTTT 7800
 Qy 7801 TTTCCCTTT 7860
 Db 7801 TTTCCCTTT 7860
 Qy 7861 TTTTCTCTTT 7920
 Db 7861 TTTTCTCTTT 7920
 Qy 7921 TAGCTGTAAAGGTCCTGAGCGGCTTGAAGTGTGAGAGTGTGATGATGCTGCTCTGCG 7980
 Db 7921 TAGCTGTAAAGGTCCTGAGCGGCTTGAAGTGTGAGAGTGTGATGATGCTGCTCTGCG 7980

Qy 7981 AGATCAAGTACT 7992
 Db 7981 AGATCAAGTACT 7992

RESULT 15

AAL47279
 ID AAL47279 standard; DNA; 7991 BP.

XX AAL47279;

XX 30-AUG-2002 (first entry)

XX Hepatitis C virus sub-genomic replicon recombinant clone HCVr9.

XX Hepatitis; HCV; core-neo; NS3 proteinase/helicase; vaccine; diagnosis;
 KW virucide; hepatotropic; gene therapy; anti-viral; gene; ds.

XX Hepatitis C virus.

XX WO200238793-A2.

XX 16-MAY-2002.

XX 02-NOV-2001; 2001WO-US046350.

XX 07-NOV-2000; 2000US-0245866P.

XX (ANAD-) ANADYS PHARM INC.

XX Bichko V;

XX WPI; 2002-490082/52.

XX Novel nucleic acid encoding replication competent recombinant hepatitis C
 PT virus genome useful for screening anti-hepatitis C virus therapeutics and
 PT for vaccine development.

XX Claim 9; Page 61-65; 85pp; English.

XX The present invention provides protein and coding sequences from
 CC Hepatitis C virus (HCV), comprising all or part of the HCV genome and
 CC able to replicate efficiently when transfected into a susceptible cell
 CC line without reducing the growth rate of the cell line by more than 10
 CC fold. The sequences are useful for screening for anti-HCV therapeutics,
 CC for detecting antibodies to HCV in a biological sample such as blood,
 CC serum, plasma, blood cells, lymphocytes, or liver cells from a subject,
 CC for deriving authentic HCV components such as replication-competent non-
 CC infectious, replication-defective infection-component, and replication-
 CC defective non-infectious HCV, in gene therapy or gene vaccination
 CC targeted to hepatic tissue for treating an animal infected or susceptible
 CC to HCV infection and for studying HCV infection and propagation. The
 CC present sequence is a clone of a fragment of the HCV genome designated
 CC HCVr9

XX Sequence 7991 BP; 1647 A; 2369 C; 2245 G; 1730 T; 0 U; 0 Other;

XX Query Match 99.8%; Score 7980; DB 6; Length 7991;

XX Best Local Similarity 100.0%; Pred. No. 0;

XX Matches 7991; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 GCCAGCCCCCGATTGGGGGAGACACTCCACATAGATCACTCCCTGTGAGAACTACTG 60

Db 1 GCCAGCCCCCGATTGGGGGAGACACTCCACATAGATCACTCCCTGTGAGAACTACTG 60

Qy 61 TCTTCAAGCAGAAAGCGTCTAGCATCGCTTAGTATGATGATGATGATGATGATGATGATG 120

Db 61 TCTTCAAGCAGAAAGCGTCTAGCATCGCTTAGTATGATGATGATGATGATGATGATGATG 120

Qy 121 CCCCCTCCCGGGAGAGCCATAGTGTCTCGGAACCGGTGAGTACACCGGAATTGCCAG 180

Db 121 CCCCCTCCCGGGAGAGCCATAGTGTCTCGGAACCGGTGAGTACACCGGAATTGCCAG 180

QY 181 GACGACCGGGTCTTTCTTGGATCAACCGCTCAATGCTGTGAGATTTGGGGTGCCTCC 240
DB 181 GACGACCGGGTCTTTCTTGGATCAACCGCTCAATGCTGTGAGATTTGGGGTGCCTCC 240
QY 241 GCGAGACTGTAGCGAGTAGTGTGGGTGCGGAAAGCGCTTGTGTAATGCTGATAGG 300
DB 241 GCGAGACTGTAGCGAGTAGTGTGGGTGCGGAAAGCGCTTGTGTAATGCTGATAGG 300
QY 301 GTGCTTGGAGTGGCCCGGAGTCTCGTAGACCGTGCACCAATGAGCAGMAATCCTAAG 360
DB 301 GTGCTTGGAGTGGCCCGGAGTCTCGTAGACCGTGCACCAATGAGCAGMAATCCTAAG 360
QY 361 CTCGAGGAAAAACAAAGGCGCGCATGATTTGAACAAGATGGAATGCAACGAGGTCTTC 420
DB 361 CTCGAGGAAAAACAAAGGCGCGCATGATTTGAACAAGATGGAATGCAACGAGGTCTTC 420
QY 421 CGCGCGTGTGGTGAGAGGCTATTGCGCTATGACTGGGCAACACAGACAATCGGCTGCT 480
DB 421 CGCGCGTGTGGTGAGAGGCTATTGCGCTATGACTGGGCAACACAGACAATCGGCTGCT 480
QY 481 CTGATCGCGCGTGTTCGGCTGTGACGCGAGGGCGCGCGTCTTTTGTCAAGACCG 540
DB 481 CTGATCGCGCGTGTTCGGCTGTGACGCGAGGGCGCGCGTCTTTTGTCAAGACCG 540
QY 541 ACCTGTCCGCTGCGCTGAATGAACTGACGAGCAGAGCGAGCGGCTATCGTGGCTGGCCA 600
DB 541 ACCTGTCCGCTGCGCTGAATGAACTGACGAGCAGAGCGAGCGGCTATCGTGGCTGGCCA 600
QY 601 CGACGGGGTTCCTTGGCGAGCTGTGCTGAGAGTGTGCTGACAGCGGGAAGGAGTGGC 660
DB 601 CGACGGGGTTCCTTGGCGAGCTGTGCTGAGAGTGTGCTGACAGCGGGAAGGAGTGGC 660
QY 661 TGCTATTGGGGAAGTGCAGGCGAGGATCTCTGTGATCTCACTTGTCTGCTGCGGAGA 720
DB 661 TGCTATTGGGGAAGTGCAGGCGAGGATCTCTGTGATCTCACTTGTCTGCTGCGGAGA 720
QY 721 AAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACGCTTGTGCTGCGGCTACCTGCC 780
DB 721 AAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACGCTTGTGCTGCGGCTACCTGCC 780
QY 781 CATTCGACCAAGCGGAAATCGCATCGAGCAGCAGCTACTCGGATGGAAGCGGTC 840
DB 781 CATTCGACCAAGCGGAAATCGCATCGAGCAGCAGCTACTCGGATGGAAGCGGTC 840
QY 841 TTGTGATCAGGATGATCTGCAAGAGCATCAGGGGCTCGCGCCAGCGAACTGTTCG 900
DB 841 TTGTGATCAGGATGATCTGCAAGAGCATCAGGGGCTCGCGCCAGCGAACTGTTCG 900
QY 901 CCAGGCTCAAGGCGCATGCGGCGAGGATCTCGTCTGAGCAGCATGCGGATGCGGATGCT 960
DB 901 CCAGGCTCAAGGCGCATGCGGCGAGGATCTCGTCTGAGCAGCATGCGGATGCGGATGCT 960
QY 961 GCTTGGCAATATATGCTGGAATATGGCGCTTCTGCAATCATCGACTGGCGGC 1020
DB 961 GCTTGGCAATATATGCTGGAATATGGCGCTTCTGCAATCATCGACTGGCGGC 1020
QY 1021 TGCGGTGCGGACCGCTATCAGACATAGCGTGGCTACCGGTGATTTGCTGAGAGC 1080
DB 1021 TGCGGTGCGGACCGCTATCAGACATAGCGTGGCTACCGGTGATTTGCTGAGAGC 1080
QY 1081 TTGGCGGCAATGGGCTGACCGCTTCTGCTGCTTACGGTATCGCGCTCCCGATTCG 1140
DB 1081 TTGGCGGCAATGGGCTGACCGCTTCTGCTGCTTACGGTATCGCGCTCCCGATTCG 1140
QY 1141 AGCGCATCGCTTCTATCGCTTCTGACAGTCTTCTGAGTTTAAACAGACCAACAG 1200
DB 1141 AGCGCATCGCTTCTATCGCTTCTGACAGTCTTCTGAGTTTAAACAGACCAACAG 1200
QY 1201 GTTTCCTCTAGCGGATCAATTCGCGCTCTCCCTCCCGCTTAAAGTACTGGC 1260
DB 1201 GTTTCCTCTAGCGGATCAATTCGCGCTCTCCCTCCCGCTTAAAGTACTGGC 1260

QY 1261 CGAAGCGCTTGGATTAAGCGCGTGTGCGTTTGTCTATATGTTATTTTCCACCATATG 1320
DB 1261 CGAAGCGCTTGGATTAAGCGCGTGTGCGTTTGTCTATATGTTA-TTTCACCATATG 1319
QY 1321 CCGTCTTTTGGCAATGTGAGGCGCGGAAACCTGCCCTGTCTTCTTGAAGCAATCT 1380
DB 1320 CCGTCTTTTGGCAATGTGAGGCGCGGAAACCTGCCCTGTCTTCTTGAAGCAATCT 1379
QY 1381 AGGGTCTTTTCCCTCTCGCAAGGAATGCAAGGTCTGTGAAATGCTGTGAAGCAAC 1440
DB 1380 AGGGTCTTTTCCCTCTCGCAAGGAATGCAAGGTCTGTGAAATGCTGTGAAGCAAC 1439
QY 1441 GTTCTCTGGAAGCTTCTTGAAGCAACCAAGCTCTGTAGCAACCTTGTGAGGAGCG 1500
DB 1440 GTTCTCTGGAAGCTTCTTGAAGCAACCAAGCTCTGTAGCAACCTTGTGAGGAGCG 1499
QY 1501 AACCCCGCTTGGCGAGCTCTCGCGGCAAGGCTGTAAGATACCT 1560
DB 1500 AACCCCGCTTGGCGAGCTCTCGCGGCAAGGCTGTAAGATACCT 1559
QY 1561 GCAAGGCGGCAACCCAGTGTGAGTGTGAAAGAGTCAAA 1620
DB 1560 GCAAGGCGGCAACCCAGTGTGAGTGTGAAAGAGTCAAA 1619
QY 1621 TGGCTCTCTCAAGGCTATTCAACAGGGGCTGAGGATGCCAGAGGTACCCCATGT 1680
DB 1620 TGGCTCTCTCAAGGCTATTCAACAGGGGCTGAGGATGCCAGAGGTACCCCATGT 1679
QY 1681 ATGGGATCTGATCTGGGCTCTCGGTGCACATGCTTACATGCTTGTAGTTCGAGGTAAA 1740
DB 1680 ATGGGATCTGATCTGGGCTCTCGGTGCACATGCTTACATGCTTGTAGTTCGAGGTAAA 1739
QY 1741 AACCTCTAGGCGGCGGAGCTGCTTCTTGAAGCAACGATAAAC 1800
DB 1740 AACCTCTAGGCGGCGGAGCTGCTTCTTGAAGCAACGATAAAC 1799
QY 1801 ATGGCGCTATTAGGCTTACTCCACAGAGCGGAGCTTGTGGCTGATCATCACT 1860
DB 1800 ATGGCGCTATTAGGCTTACTCCACAGAGCGGAGCTTGTGGCTGATCATCACT 1859
QY 1861 AGCTCACAGCGCGGAGCAAGGCTCGAGGGAGGTCAGAGTGTCTCCACGCA 1920
DB 1860 AGCTCACAGCGCGGAGCAAGGCTCGAGGGAGGTCAGAGTGTCTCCACGCA 1919
QY 1921 ACAATCTTCTTGGCGACTGCTCAATGCGCTGTGTGGAGTGTCTATCATGTGCC 1980
DB 1920 ACAATCTTCTTGGCGACTGCTCAATGCGCTGTGTGGAGTGTCTATCATGTGCC 1979
QY 1981 GGCTCAAGACCTTGGCGGCGGCAAGGCGGCAATCAACCAATGTACCAATGTGGAC 2040
DB 1980 GGCTCAAGACCTTGGCGGCGGCAAGGCGGCAATCAACCAATGTACCAATGTGGAC 2039
QY 2041 CAGGACTCTGCTGGCAAGCGGCGGCGGCTTGTGAGCAGCTTGTGAGCAGCTGTC 2100
DB 2040 CAGGACTCTGCTGGCAAGCGGCGGCGGCTTGTGAGCAGCTTGTGAGCAGCTGTC 2099
QY 2101 GGAGCTCGGACTTACTTGTGTCAGGAGCATGCGGATGTCAATCCGCTGCGCGCGG 2160
DB 2100 GGAGCTCGGACTTACTTGTGTCAGGAGCATGCGGATGTCAATCCGCTGCGCGCGG 2159
QY 2161 GGCGAGCAGGAGGAGCTTCTTCCCGAGCGCTCTCTTGAAGGGCTCTTCG 2220
DB 2160 GGCGAGCAGGAGGAGCTTCTTCCCGAGCGCTCTCTTGAAGGGCTCTTCG 2219
QY 2221 GGCGTCTACTGCTGCGGCTTGGGCGAGCTGTGGGCTTCTTGGGCTGCGGTGTC 2280
DB 2220 GGCGTCTACTGCTGCGGCTTGGGCGAGCTGTGGGCTTCTTGGGCTGCGGTGTC 2279
QY 2281 ACCGAGGGGTTGCAAGGCGGTGAGCTTTGTACCGCTGAGTGTATGGAACCACTATG 2340
DB 2280 ACCGAGGGGTTGCAAGGCGGTGAGCTTTGTACCGCTGAGTGTATGGAACCACTATG 2339
QY 2341 CGGTCCCGGCTTTCAGGAGCAACTGCTCCCTCGCGCGGTACCGGAGACATTCAGGTG 2400

Db	2340	CGGTCCCGGCTTTCACGGACAACCTGCTCCCTCGCGCGGTACCGACACATTCAGGTG	2399	Db	3420	ACCCACATAGACGCCCATTTCTTGTCCAGACTAAGCAGGAGGAGACAACCTTCCCTTAC	3479
Qy	2401	GCCCATCTACAGCCCTTACTGGTAGCGGCAAGAGCACTAAGGTGCCCGGTGCGTATGCA	2460	Qy	3481	CTGTGTAGCATACACAGGCTACGGTGTGCGCCAGGGCTCAGAGCTCCACCTTCCATCTGTGGAC	3540
Db	2400	GCCCATCTACAGCCCTTACTGGTAGCGGCAAGAGCACTAAGGTGCCCGGTGCGTATGCA	2459	Db	3480	CTGTGTAGCATACACAGGCTACGGTGTGCGCCAGGGCTCAGGCTCCACCTTCCATCTGTGGAC	3539
Qy	2461	GCCCAAGGGTATAAGGTGCTGTGCTGAACCGTCCGTCGCGCCACACCTTAGTTTCGGG	2520	Qy	3541	CAATGTGGAAAGTGTCTCATACGGGTAAAGCTTACGCTGACGGGCCAACCGCCCTGTG	3600
Db	2460	GCCCAAGGGTATAAGGTGCTGTGCTGAACCGTCCGTCGCGCCACACCTTAGTTTCGGG	2519	Db	3540	CAATGTGGAAAGTGTCTCATACGGGTAAAGCTTACGCTGACGGGCCAACCGCCCTGTG	3599
Qy	2521	GGTATATGTCTAAGGCAATGGTATCGACCCCTAAACATCAGAACCGGGTAAAGCAATC	2580	Qy	3601	TATAGCTGGGAGCGGTTCAAAACGAGGTACTACACACACCCCATAAACAAATACATC	3660
Db	2520	GGTATATGTCTAAGGCAATGGTATCGACCCCTAAACATCAGAACCGGGTAAAGCAATC	2579	Db	3600	TATAGCTGGGAGCGGTTCAAAACGAGGTACTACACACACCCCATAAACAAATACATC	3659
Qy	2581	ACCAGGGTGCCCGCATCAGTATCTCCACCTATGGAAGTCTTTCGCGACGGTGTGC	2640	Qy	3661	ATGGCATCATGTCTCGGCTGACCTGAGGTGCTCAGAGCACCTGCTGTGTAGCGGA	3720
Db	2580	ACCAGGGTGCCCGCATCAGTATCTCCACCTATGGAAGTCTTTCGCGACGGTGTGC	2639	Db	3660	ATGGCATCATGTCTCGGCTGACCTGAGGTGCTCAGAGCACCTGCTGTGTAGCGGA	3719
Qy	2641	TCTGGGGGCGCTATGACATCATATATGTGATGTCACCTCAACTGACCTCGACCT	2700	Qy	3721	GTCTAGCAGCTCTCGCGCGGTATTTGCTGACAAACAGGAGCGTGTGCTGTGGCAGG	3780
Db	2640	TCTGGGGGCGCTATGACATCATATATGTGATGTCACCTCAACTGACCTCGACCT	2699	Db	3720	GTCTAGCAGCTCTCGCGCGGTATTTGCTGACAAACAGGAGCGTGTGCTGTGGCAGG	3779
Qy	2701	ATCTGGGCATCGGACAGTCTCTGGACCAAGCGGAGACGGCTGGAGCGGACTCGTCGTG	2760	Qy	3781	ATCATCTTGTCCGGAAGCGCGCCCATCTTCCCGACAGGAAAGTCTTTTACCGGAGTTTC	3840
Db	2700	ATCTGGGCATCGGACAGTCTCTGGACCAAGCGGAGACGGCTGGAGCGGACTCGTCGTG	2759	Db	3780	ATCATCTTGTCCGGAAGCGCGCCCATCTTCCCGACAGGAAAGTCTTTTACCGGAGTTTC	3839
Qy	2761	CTCGCCACCGCTACGCTCCGGGATCGGTACCGTCCCATATCATAAATCGAGGAGGTG	2820	Qy	3841	GATGAGATGGAAGAGTGGCGCTCACACCTCCCTTACATCGAAACAGGAAATGAGCTCGCC	3900
Db	2760	CTCGCCACCGCTACGCTCCGGGATCGGTACCGTCCCATATCATAAATCGAGGAGGTG	2819	Db	3840	GATGAGATGGAAGAGTGGCGCTCACACCTCCCTTACATCGAAACAGGAAATGAGCTCGCC	3899
Qy	2821	GCTCTGTCCAGCACTGGAGAAATCCCTTTTATGGCAAGCCATCCCATCGAGACCATC	2880	Qy	3901	GAACAATTCAAACAGAAAGCAATCGGTTGCTGCAAAAGCCACCAGCAAGCGGAGGCT	3960
Db	2820	GCTCTGTCCAGCACTGGAGAAATCCCTTTTATGGCAAGCCATCCCATCGAGACCATC	2879	Db	3900	GAACAATTCAAACAGAAAGCAATCGGTTGCTGCAAAAGCCACCAGCAAGCGGAGGCT	3959
Qy	2881	AAGGGGGAGGCACTCTCTTCTGCCATTCGAAAGAAATGTGATGAGCTCGCGCGG	2940	Qy	3961	GCTGCTCCGCTGTGGAATCCCAAGTGGCGGACCTCTGAAAGCCCTTCTGGCGAAGCATATG	4020
Db	2880	AAGGGGGAGGCACTCTCTTCTGCCATTCGAAAGAAATGTGATGAGCTCGCGCGG	2939	Db	3960	GCTGCTCCGCTGTGGAATCCCAAGTGGCGGACCTCTGAAAGCCCTTCTGGCGAAGCATATG	4019
Qy	2941	AAGCTGTCCGGCTCGGACTCAATGTGTAGCATATTAACGGGGCTTGATGATCGGTC	3000	Qy	4021	TGGAAATTCATCAGCGGGATACAATATTTAGCAGGCTTGTCCAATCTGTGCTGCAACCCC	4080
Db	2940	AAGCTGTCCGGCTCGGACTCAATGTGTAGCATATTAACGGGGCTTGATGATCGGTC	2999	Db	4020	TGGAAATTCATCAGCGGGATACAATATTTAGCAGGCTTGTCCAATCTGTGCTGCAACCCC	4079
Qy	3001	ATACCAACTAGCGAGACGTCATGTCGTAGCAACGACGCTCTAATAGCGGCTTACC	3060	Qy	4081	GCATAGATCACTGATGGCATTCACAGCTCTATCACCAGCGGCTCACCACCCACAT	4140
Db	3000	ATACCAACTAGCGAGACGTCATGTCGTAGCAACGACGCTCTAATAGCGGCTTACC	3059	Db	4080	GCATAGATCACTGATGGCATTCACAGCTCTATCACCAGCGGCTCACCACCCACAT	4139
Qy	3061	GGCGATTCGACTCAGTGTACGACTGCAATACATGTGTACCCAGACAGTCTCAGC	3120	Qy	4141	ACCTCTCTGTTTAAACATCTCTGGGGGATGGGTGGCGGCCCAACTTGTCTCTCCAGCGCT	4200
Db	3060	GGCGATTCGACTCAGTGTACGACTGCAATACATGTGTACCCAGACAGTCTCAGC	3119	Db	4140	ACCTCTCTGTTTAAACATCTCTGGGGGATGGGTGGCGGCCCAACTTGTCTCTCCAGCGCT	4199
Qy	3121	CTGACCCGACCTTACCATGTAGAGACGACCGTGTGCAAGACCGGTGTCAACGCTG	3180	Qy	4201	GCTTCTGCTTCTGAGCGCGGCTATGCTGTGGAGGGCTTGTGGAGCATAGGCTTGGG	4260
Db	3120	CTGACCCGACCTTACCATGTAGAGACGACCGTGTGCAAGACCGGTGTCAACGCTG	3179	Db	4200	GCTTCTGCTTCTGAGCGCGGCTATGCTGTGGAGGGCTTGTGGAGCATAGGCTTGGG	4259
Qy	3181	CAGCGGAGGAGGAGTGTGAGGGGAGGATGGGCAATTTACAGTTTGTGACTCCAGGA	3240	Qy	4261	AAGGTGCTGTGATATTTTGGCAGGTATGAGAGCAGGGGTGGCAGCGCGCTGTGCGC	4320
Db	3180	CAGCGGAGGAGGAGTGTGAGGGGAGGATGGGCAATTTACAGTTTGTGACTCCAGGA	3239	Db	4260	AAGGTGCTGTGATATTTTGGCAGGTATGAGAGCAGGGGTGGCAGCGCGCTGTGCGC	4319
Qy	3241	GAACGGGCTTCCGGCATGTTCCGATTCCTCGTTCCTGTGCGAGTGTATGACGGGGTGT	3300	Qy	4321	TTTAAAGTCAATGAGCGCGGATGCCCTCCACCGAGGACCTTGGCTAACTTCTCTCTGCT	4380
Db	3240	GAACGGGCTTCCGGCATGTTCCGATTCCTCGTTCCTGTGCGAGTGTATGACGGGGTGT	3299	Db	4320	TTTAAAGTCAATGAGCGCGGATGCCCTCCACCGAGGACCTTGGCTAACTTCTCTCTGCT	4379
Qy	3301	GCTTGTGACAGCTCAGCGCGCGGAGACCTCAGTTAGGTGCGGCTTACCTTAAACACA	3360	Qy	4381	ATCCTCTCCCTGGCGCCCTAGTGTGCTGGAGGGTGTGCGAGGAGTATGCTGCTGCGAC	4440
Db	3300	GCTTGTGACAGCTCAGCGCGCGGAGACCTCAGTTAGGTGCGGCTTACCTTAAACACA	3359	Db	4380	ATCCTCTCCCTGGCGCCCTAGTGTGCTGGAGGGTGTGCTGCGAGGAGTATGCTGCTGCGAC	4439
Qy	3361	CCAGGTTGCCGCTGCGAGGACCATCTGAGTTCTGGAGAGCGCTTTTACAGGCGTC	3420	Qy	4441	GTGGGCGGAGGAGGGGCTGTGCACTGATGAACCGGCTGTAGAGGTTGCTTCCCGG	4500
Db	3360	CCAGGTTGCCGCTGCGAGGACCATCTGAGTTCTGGAGAGCGCTTTTACAGGCGTC	3419	Db	4440	GTGGGCGGAGGAGGGGCTGTGCACTGATGAACCGGCTGTAGAGGTTGCTTCCCGG	4499
Qy	3421	ACCACATAGACGCCCATTTCTTGTCCAGACTAAGCAGGAGGAGACAACCTTCCCTTAC	3480	Qy	4501	GGTAAACACAGCTCTCCCCCAGCAGCTATGTGCTGTAGAGCGGAGCGCTGTGAGCAGCTGTCACT	4560
Db				Db	4500	GGTAAACACAGCTCTCCCCCAGCAGCTATGTGCTGTAGAGCGGAGCGCTGTGAGCAGCTGTCACT	4559

Db 6720 CCGAAGCCAGACAGCCCATAGGTCGCTCAGAGCGGCTTACATCGGGGCCCCCTG 6779
Qy 6781 ACTAATTTCTAAGGGCAGAACTGGCGCTATCGCCGTCGCGAGCGGTGTACTGACG 6840
Db 6780 ACTAATTTCTAAGGGCAGAACTGGCGCTATCGCCGTCGCGAGCGGTGTACTGACG 6839
Qy 6841 ACCAGCTCGGTAAATACCTCATGTTACTTTGAAGCGCGCTGCGCCCTGTGAGCTGG 6900
Db 6840 ACCAGCTCGGTAAATACCTCATGTTACTTTGAAGCGCGCTGCGCCCTGTGAGCTGG 6899
Qy 6901 AAGCTCCAGGACTGACAGATGCTCTGATGCGAGACGACCTTGTCTGTTATCTGTAAGC 6960
Db 6900 AAGCTCCAGGACTGACAGATGCTCTGATGCGAGACGACCTTGTCTGTTATCTGTAAGC 6959
Qy 6961 GCGGGGACCCAGAGAGCAGGCGAGCTTACGGGCTTACAGGAGCTATGACTAGATAC 7020
Db 6960 GCGGGGACCCAGAGAGCAGGCGAGCTTACGGGCTTACAGGAGCTATGACTAGATAC 7019
Qy 7021 TCTGCCCCCTTGGGGAACCGGCCAAACAGAAATAGGACTTGGAGTTGATACATCATGC 7080
Db 7020 TCTGCCCCCTTGGGGAACCGGCCAAACAGAAATAGGACTTGGAGTTGATACATCATGC 7079
Qy 7081 TCTTCCAAATGTCTAGTCGCGACGATGCTTGGCAAAAGGTGTACTATCTCACCCGT 7140
Db 7080 TCTTCCAAATGTCTAGTCGCGACGATGCTTGGCAAAAGGTGTACTATCTCACCCGT 7139
Qy 7141 GACCCACACCCCTTGGCGGGCTGCGTGGGAGACAGCTAGACACACTCCAGTCAAT 7200
Db 7140 GACCCACACCCCTTGGCGGGCTGCGTGGGAGACAGCTAGACACACTCCAGTCAAT 7199
Qy 7201 TCTGCTAGGCAACATCATGATGATGCGCCACCTTGGSCAAGGATGATCCTGATG 7260
Db 7200 TCTGCTAGGCAACATCATGATGCGCCACCTTGGSCAAGGATGATCCTGATG 7259
Qy 7261 ACTCATTTCTTCCATCTTCTAGCTCAGGAACAACTTGAAGGACCTTAGATTCTCAG 7320
Db 7260 ACTCATTTCTTCCATCTTCTAGCTCAGGAACAACTTGAAGGACCTTAGATTCTCAG 7319
Qy 7321 ATCTAGGGGCTGTATCTCCATGAGCCACTTGACCTCAGATCATTCACGACTC 7380
Db 7320 ATCTAGGGGCTGTATCTCCATGAGCCACTTGACCTCAGATCATTCACGACTC 7379
Qy 7381 CATGGCTTAGCCGATTTTCACTCCATGATTTACTCTCCAGGTGAGATCAATAGGGTGGCT 7440
Db 7380 CATGGCTTAGCCGATTTTCACTCCATGATTTACTCTCCAGGTGAGATCAATAGGGTGGCT 7439
Qy 7441 TCATGCTCAGGAAACTTGGGGTACCGCCCTTGGAGTCTGGAGACATCGGGCCAGAAAT 7500
Db 7440 TCATGCTCAGGAAACTTGGGGTACCGCCCTTGGAGTCTGGAGACATCGGGCCAGAAAT 7499
Qy 7501 GTCGCGCTAGGCTACTGTCCAGGGGGGAGGGCTGCCACTTGTGGCAAGTACTCTTC 7560
Db 7500 GTCGCGCTAGGCTACTGTCCAGGGGGGAGGGCTGCCACTTGTGGCAAGTACTCTTC 7559
Qy 7561 AACTGGGAGTAGGACCAAGCTCAACTCACTCCATCCGCGTCCGCTCCAGTTGGAT 7620
Db 7560 AACTGGGAGTAGGACCAAGCTCAACTCACTCCATCCGCGTCCGCTCCAGTTGGAT 7619
Qy 7621 TTATCCAGCTGGTTCTGTTGTTACGCGGGGAGACATATATACAGCCCTGTCTCGT 7680
Db 7620 TTATCCAGCTGGTTCTGTTGTTACGCGGGGAGACATATATACAGCCCTGTCTCGT 7679
Qy 7681 GCGGACCCGCTGGTTCTGTTGTTGCTTACTCTTCTGTTAGGGGTAGGCATCTAT 7740
Db 7680 GCGGACCCGCTGGTTCTGTTGTTGCTTACTCTTCTGTTAGGGGTAGGCATCTAT 7739
Qy 7741 CTACTCCCAACCGATGAACGGGAGCTTAAACACTCCAGGCAATAGGCCATCTCTTTT 7800
Db 7740 CTACTCCCAACCGATGAACGGGAGCTTAAACACTCCAGGCAATAGGCCATCTCTTTT 7799
Qy 7801 TTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7860

Db 7800 TTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7859
Qy 7861 TTTTTCCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7920
Db 7860 TTTTTCCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7919
Qy 7921 TAGCTGTGAAAGGTCCGTGAGCCGTTGACTGCGAGAGAGTGTGATACCTGGCCTCTCTGC 7980
Db 7920 TAGCTGTGAAAGGTCCGTGAGCCGTTGACTGCGAGAGAGTGTGATACCTGGCCTCTCTGC 7979
Qy 7981 AGATCAAGTACT 7992
Db 7980 AGATCAAGTACT 7991

Search completed: August 12, 2004, 04:08:49
Job time : 1852 secs

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OM nucleic - nucleic search, using sw model

Run on: August 12, 2004, 03:20:41 ; Search time 12010 Seconds

(without alignments)

19871.653 Million cell updates/sec

Title:

US-10-005-469-4

Perfect score: 7992

Sequence: 1 gccagcccgattgggggc.....ctctctgcagatcaagtact 7992

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.*

1: em_estba.*

2: em_esthum.*

3: em_estin.*

4: em_estnu.*

5: em_estov.*

6: em_estpl.*

7: em_estro.*

8: em_estc.*

9: gb_est1.*

10: gb_est2.*

11: gb_est3.*

12: gb_est4.*

13: gb_est5.*

14: gb_est6.*

15: em_estfun.*

16: em_estom.*

17: em_gss_hum.*

18: em_gss_inv.*

19: em_gss_pln.*

20: em_gss_vrt.*

21: em_gss_fun.*

22: em_gss_mam.*

23: em_gss_mus.*

24: em_gss_pro.*

25: em_gss_rod.*

26: em_gss_phg.*

27: em_gss_vrl.*

28: gb_gss1.*

29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	795.4	10.0	935	14	CK284786
2	794	9.9	804	14	CK291519
3	794	9.9	856	14	CK287297
4	794	9.9	910	14	CK287930

5	794	9.9	933	14	CK291799	CK291799 EST754513
6	794	9.9	936	14	CK256977	CK256977 EST740614
7	794	9.9	947	14	CK298208	CK298208 EST760922
8	794	9.9	954	14	CK283361	CK283361 EST746083
9	778.8	9.7	811	14	CK288185	CK288185 EST750907
10	587	7.3	878	14	CK288711	CK288711 EST751433
11	577.4	7.2	789	28	AQ361914	AQ361914 mgxb0005K
12	559.8	7.0	620	28	AQ398387	AQ398387 mgxb0009J
13	514.8	6.4	561	28	AQ447874	AQ447874 mgxb0012I
14	508	6.3	509	28	AQ447775	AQ447775 mgxb0011E
15	505.4	6.3	637	28	AQ447230	AQ447230 mgxb0006O
16	503.8	6.3	592	28	AQ449162	AQ449162 mgxb0023E
17	499	6.2	499	28	AQ398880	AQ398880 mgxb0006P
18	486.4	6.2	498	28	AQ398730	AQ398730 mgxb0009G
19	475.8	6.0	857	28	AQ875013	AQ875013 V120B8 mt
20	474.8	5.9	710	28	BH972732	BH972732 odj46h10.
21	469.8	5.9	473	28	AQ397768	AQ397768 mgxb0001J
22	468.8	5.9	594	28	AQ397253	AQ397253 mgxb0003C
23	465.2	5.8	850	28	AQ875052	AQ875052 V120F5 mt
24	463.4	5.8	798	28	AQ876139	AQ876139 V133G10 m
25	458.8	5.7	482	9	AL449872	AL449872 AL449872
26	456.8	5.7	861	28	AQ875040	AQ875040 V120E4 mt
27	455.6	5.7	815	28	AQ876134	AQ876134 V133F5 mt
28	451.2	5.6	799	28	AQ876220	AQ876220 V152G7 mt
29	450	5.6	784	28	AQ876152	AQ876152 V133H12 m
30	444.6	5.6	790	28	AQ875904	AQ875904 V130H11 m
31	437.2	5.5	797	28	AQ876297	AQ876297 V153G3 mt
32	434.6	5.4	765	14	CK283362	CK283362 EST746084
33	426.8	5.3	804	28	AQ876080	AQ876080 V133A4 mt
34	422.8	5.3	759	14	CK298209	CK298209 EST760923
35	414.6	5.2	791	28	AQ876019	AQ876019 V132C3 mt
36	409.4	5.1	748	28	AQ501530	AQ501530 V20F6 mtN
37	408	5.1	635	28	AQ447643	AQ447643 mgxb0008M
38	408	5.1	656	28	AQ447140	AQ447140 mgxb0005I
39	404	5.1	790	28	AQ875912	AQ875912 V130H8 mt
40	404	5.1	791	28	AQ876201	AQ876201 V152B2 mt
41	402.6	5.0	856	28	AQ875050	AQ875050 V120F2 mt
42	401.8	5.0	760	14	CK287931	CK287931 EST750653
43	398.8	5.0	722	14	CD641598	CD641598 AGENCOURT
44	398	5.0	734	28	AQ873679	AQ873679 V73F2 mtN
45	396.6	5.0	801	28	AQ876288	AQ876288 V153F3 mt

ALIGNMENTS

RESULT 1
CK284786

LOCUS

DEFINITION

EST747508 Nicotiana benthamiana mixed tissue cDNA library,

normalized, full-length Nicotiana benthamiana cDNA clone NBMAQ41 5'

end, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Nicotiana benthamiana

Nicotiana benthamiana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

asterids; lamiales; Solanales; Solanaceae; Nicotiana.

1 (bases 1 to 935)

Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A., Day,B.,

Staskiewicz,B., Jin,H. and Baker,B.

Generation of EST sequences from Nicotiana benthamiana

Unpublished (2003)

Other ESTs: EST747509

Contact: Robin Buell

The Institute for Genomic Research

9712 Medical Center Dr, Rockville, MD 20850, USA

Email: potato-array@tigr.org

Clones can be requested from TIGR via potato@tigr.org

Seq primer: ATT TAG GTG ACA CTA TAG.

Location/Qualifiers

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source
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/organism="Nicotiana benthamiana"
/mol_type="mRNA"
/db_xref="taxon:4100"
/clone="NEMA041"
/tissue_type="abiotic and biotic stress-treated leaves, callus tissue and root tissue"
/lab_host="DH10B-Tona"
/clone_lib="Nicotiana benthamiana mixed tissue cDNA library, normalized, full-length"
/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI; tissues that include callus, roots from liquid culture grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr), cold-stressed leaves (5 C 3 hr, 6hr), and pathogen challenged leaves (Pseudomonas syringae pv tomato 12 hr; Xanthomonas campestris pv campestris 12 hr, 18hr; Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas campestris pv vesicatoria 18hr). RNA was isolated from these tissues and pooled in approximately equal molar amounts."

ORIGIN
Query Match 10.0%; Score 795.4; DB 14; Length 935;
Best Local Similarity 99.9%; Pred. No. 6.1e-108; Indels 0; Gaps 0;
Matches 796; Conservative 0; Mismatches 1;

QY 386 CATGATTCAACAAGATGATTGCAGCGAGTTCTCCGGCCGCTTGGGTGGAGAGCTATT 445
DB 31 CATGATTCAACAAGATGATTGCAGCGAGTTCTCCGGCCGCTTGGGTGGAGAGCTATT 90
QY 446 CGGCTATGACTGGGCACACAGACAATCGGTGCTCTGATGCGCGCTGTTCCGGCTGTC 505
DB 91 CGGCTATGACTGGGCACACAGACAATCGGTGCTCTGATGCGCGCTGTTCCGGCTGTC 150
QY 506 AGCGCAGGGCGCGCGCTTTTGTCAAGCCAGCTGTCGGTGGCTCGTAATGAAT 565
DB 151 AGCGCAGGGCGCGCGCTTTTGTCAAGCCAGCTGTCGGTGGCTCGTAATGAAT 210
QY 566 GCAGCAGGAGGCGCGCTATCTGGCTGCGCACAGCGCGCTTCTTGGCGAGCTGT 625
DB 211 GCAGCAGGAGGCGCGCTATCTGGCTGCGCACAGCGCGCTTCTTGGCGAGCTGT 270
QY 626 GCTCAGCGTTGTCACTGAAGCGGGAAGGACTGGTCTATTTGGGGGAAGTCCGGGCA 685
DB 271 GCTCAGCGTTGTCACTGAAGCGGGAAGGACTGGTCTATTTGGGGGAAGTCCGGGCA 330
QY 686 GGAATCTCTGTCTACCTTGTCTCTGCGGAGAAAGTATCCATCATGGCTGATCAAT 745
DB 331 GGAATCTCTGTCTACCTTGTCTCTGCGGAGAAAGTATCCATCATGGCTGATCAAT 390
QY 746 GCGCGGCTGATAGCTTGTATCGGCTACCTGCCCATTCGACCAACGAGGAAACATCG 805
DB 391 GCGCGGCTGATAGCTTGTATCGGCTACCTGCCCATTCGACCAACGAGGAAACATCG 450
QY 806 CATCGAGCAGCAGCTACTCGGATGAAGCGGCTTGTGATCAGATGATCTGACCA 865
DB 451 CATCGAGCAGCAGCTACTCGGATGAAGCGGCTTGTGATCAGATGATCTGACCA 510
QY 866 AGAGCATCAGGCGCTCGCGCAGCGCACTGTTGCGCAGGCTCAAGCGCGCATGCCGA 925
DB 511 AGAGCATCAGGCGCTCGCGCAGCGCACTGTTGCGCAGGCTCAAGCGCGCATGCCGA 570
QY 926 CGCGCAGGATCTCGTGTGACCCATGCGGATGCTGCTTCCGGAATATCATGTTGGA 985
DB 571 CGCGCAGGATCTCGTGTGACCCATGCGGATGCTGCTTCCGGAATATCATGTTGGA 630
QY 986 TGGCGGCTTTTCTGGAATCATGATGCTGCGCGGCTGGGTGTGCGGACCGCTATCAG 1045
DB 631 TGGCGGCTTTTCTGGAATCATGATGCTGCGCGGCTGGGTGTGCGGACCGCTATCAG 690
QY 1046 CATAGCGTTGCTACCGGTGATATTGCTGAAGAGCTTGGCGGCGGAATGGGCTGACCG 1105

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DB 691 CATAGCGTTGGCTACCGGTGATTTCTGTAAGAGCTTGGCGGAGTGGCTGACCGCTT 750
QY 1106 CTTCTGCTTTTACGGTATCGCGCTCCCGATTCGCGAGCATCGCTTCTATCGCTTCT 1165
DB 751 CTTCTGCTTTTACGGTATCGCGCTCCCGATTCGCGAGCATCGCTTCTATCGCTTCT 810
QY 1166 TGACGAGTTTCTTCTGAG 1182
DB 811 TGACGAGTTTCTTCTGAG 827

RESULT 2
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LOCUS EST754233 Nicotiana benthamiana mixed tissue cDNA library,
DEFINITION normalized, full-length Nicotiana benthamiana cDNA clone NBMC276 5'
end, mRNA sequence.
ACCESSION CK291519
VERSION CK291519.1 GI:39872047
KEYWORDS EST.
SOURCE Nicotiana benthamiana
ORGANISM Nicotiana benthamiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 804)
Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A., Day,B.,
Staskiewicz,B., Jin,H. and Baker,B.
Generation of EST sequences from Nicotiana benthamiana
Unpublished (2003)
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: ATT TAG GTG ACA CTA TAG.

FEATURES
Location/Qualifiers
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/organism="Nicotiana benthamiana"
/mol_type="mRNA"
/db_xref="taxon:4100"
/clone="NBMC276"
/tissue_type="abiotic and biotic stress-treated leaves, callus tissue and root tissue"
/lab_host="DH10B-Tona"
/clone_lib="Nicotiana benthamiana mixed tissue cDNA library, normalized, full-length"
/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI; tissues that include callus, roots from liquid culture grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr), cold-stressed leaves (5 C 3 hr, 6hr), and pathogen challenged leaves (Pseudomonas syringae pv tomato 12 hr; Xanthomonas campestris pv campestris 12 hr, 18hr; Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas campestris pv vesicatoria 18hr). RNA was isolated from these tissues and pooled in approximately equal molar amounts."

ORIGIN
Query Match 9.9%; Score 794; DB 14; Length 804;
Best Local Similarity 100.0%; Pred. No. 1e-107; Indels 0; Gaps 0;
Matches 794; Conservative 0; Mismatches 0;

QY 389 GATTGAACAGATGGATTGACGAGCTTCTCCGGCGGCTTGGGTGGAGAGCTATTCCG 448
DB 2 GATTGAACAGATGGATTGACGAGCTTCTCCGGCGGCTTGGGTGGAGAGCTATTCCG 61
QY 449 CTATGACTGGGCAACACAGCAATCGGCTGCTCTGATCCCGCTGTTCCGGCTGTCAGC 508
DB 62 CTATGACTGGGCAACACAGCAATCGGCTGCTCTGATCCCGCTGTTCCGGCTGTCAGC 121
QY 509 GCAGGGGCGCGCGCTTCTTTTGTCAAGACCGACCTGTCGGTGCCTGTAATGAATGCA 568

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Db	122	GCAGGGGCGCGCGTCTTTTGTCAAGACCGACCTGTCCGGTGCCTGAATGAATGCA	181
QY	569	GGACGAGGACGCGGCTATCGTGGCTGGCCACGACGGGGGTTCTTGGCCAGCTGTGCT	628
Db	182	GGACGAGGACGCGGCTATCGTGGCTGGCCACGACGGGGGTTCTTGGCCAGCTGTGCT	241
QY	629	CGACGTTGTTCACCTGAAGCGGGAAGGACTGGCTGCTATTTCGGCGAAGTCCGGGGCAGGA	688
Db	242	CGACGTTGTTCACCTGAAGCGGGAAGGACTGGCTGCTATTTCGGCGAAGTCCGGGGCAGGA	301
QY	689	TTCCTGTGATCATCTGCTCTCTGCGGAGAAAGTATCCATCATGCTGATGCAATGCG	748
Db	302	TTCCTGTGATCATCTGCTCTCTGCGGAGAAAGTATCCATCATGCTGATGCAATGCG	361
QY	749	GGGGCTGTCATACCTTGATCCGGCTACCTGCCATTTCGACCAACGAGGAAATCGCAT	808
Db	362	GGGGCTGTCATACCTTGATCCGGCTACCTGCCATTTCGACCAACGAGGAAATCGCAT	421
QY	809	CGACGAGCAGCCTGCTGATGGAAGCGGCTCTTGTGATCAGATGATCTGACCAAGA	868
Db	422	CGACGAGCAGCCTGCTGATGGAAGCGGCTCTTGTGATCAGATGATCTGACCAAGA	481
QY	869	GCATCAGGGGCTCGCCGACCGAATGTTGCGCAGGCTCAAGCGCGCATGCCGACGG	928
Db	482	GCATCAGGGGCTCGCCGACCGAATGTTGCGCAGGCTCAAGCGCGCATGCCGACGG	541
QY	929	CGAGGATCTGCTGTCACCCATGCGCATGCTGCTTGGCGGACCGCTATCAGGACAT	988
Db	542	CGAGGATCTGCTGTCACCCATGCGCATGCTGCTTGGCGGACCGCTATCAGGACAT	601
QY	989	CCGCTTTTCTGATTCATCGACTGTGGCGGCTGGGTGTGGCGGACCGCTATCAGGACAT	1048
Db	602	CCGCTTTTCTGATTCATCGACTGTGGCGGCTGGGTGTGGCGGACCGCTATCAGGACAT	561
QY	1049	ACGCTTGGCTACCGTGATATGCTGAAGAGCTTGGCGGCGAATGGGCTTCTTCT	1108
Db	662	ACGCTTGGCTACCGTGATATGCTGAAGAGCTTGGCGGCGAATGGGCTTCTTCT	721
QY	1109	CGTGTCTTACGATGCGCGCTCCGATTCGAGGCTTGGCGGCGAATGGGCTTCTTGA	1168
Db	722	CGTGTCTTACGATGCGCGCTCCGATTCGAGGCTTGGCGGCGAATGGGCTTCTTGA	781
QY	1169	CGAGTTCTTCTGAG	1182
Db	782	CGAGTTCTTCTGAG	795
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LOCUS	CK287297		
DEFINITION	EST750019 Nicotiana benthamiana mixed tissue cDNA library, normalized, full-length Nicotiana benthamiana cDNA clone NBM815 5', end, mRNA sequence.		
ACCESSION	CK287297		
VERSION	CK287297.1		
KEYWORDS	EST.		
SOURCE	Nicotiana benthamiana		
ORGANISM	Nicotiana benthamiana		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Nicotiana.		
AUTHORS	Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B., Staskiewicz, B., Jin, H. and Baker, B.		
TITLE	Generation of EST sequences from Nicotiana benthamiana		
JOURNAL	Unpublished (2003)		
COMMENT	Other ESTs: EST750020		
	Contact: Robin Buell		
	The Institute for Genomic Research		
	9712 Medical Center Dr, Rockville, MD 20850, USA		
	Email: potato-array@tigr.org		
	Clones can be requested from TIGR via potato@tigr.org		

Seq primer: ATT TAG GTG ACA CTA TAG.
 Location/Qualifiers
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 /organism="Nicotiana benthamiana"
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 /db_xref="taxon:4100"
 /clone="NBM815"
 /tissue_type="abiotic and biotic stress-treated leaves, callus tissue and root tissue"
 /lab_host="DH10B-Tona"
 /clone_lib="Nicotiana benthamiana mixed tissue cDNA library, normalized, full-length"
 /note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI; supplier: RNA was isolated from Nicotiana benthamiana tissues that include callus, roots from liquid culture grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr), cold-stressed leaves (5 C 3 hr, 6hr), and pathogen challenged leaves (Pseudomonas syringae pv tomato 12 hr; Xanthomonas campestris pv campestris 12 hr, 18hr; Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas campestris pv vesicatoria 18hr). RNA was isolated from these tissues and pooled in approximately equal molar amounts."

ORIGIN

Query Match 9.9%; Score 794; DB 14; Length 856;
 Best Local Similarity 100.0%; Pred. No. 1e-107;
 Matches 794; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 389 GATTGAACAAGATGATTGCACGAGTTCTCCGCGCGCTTGGTGGAGAGGCTATTCCG 448
 Db 14 GATTGAACAAGATGATTGCACGAGTTCTCCGCGCGCTTGGTGGAGAGGCTATTCCG 73
 QY 449 CTATGACTGGGCACACAGACAATCGGCTGCTCTGATCGCGCGCTTCCGGCTGTGACG 508
 Db 74 CTATGACTGGGCACACAGACAATCGGCTGCTCTGATCGCGCGCTTCCGGCTGTGACG 133
 QY 509 GCAGGGGCGCGGTTCTTTTGTCAAGACCGACCTGTCCGGTGCCTGAATGAATGCA 568
 Db 134 GCAGGGGCGCGGTTCTTTTGTCAAGACCGACCTGTCCGGTGCCTGAATGAATGCA 193
 QY 569 GCACGAGGCGAGCGCGCTATCGTGGCTGGCCACGAGCGGCTTCTTGGCGAGCTGTGCT 628
 Db 194 GCACGAGGCGAGCGCGCTATCGTGGCTGGCCACGAGCGGCTTCTTGGCGAGCTGTGCT 253
 QY 629 CGACGTTGTCACTGAAGCGGGAAGGACTGGCTGCTATTGGCGGAAGTCCCGGCGAGGA 688
 Db 254 CGACGTTGTCACTGAAGCGGGAAGGACTGGCTGCTATTGGCGGAAGTCCCGGCGAGGA 313
 QY 689 TCTCTGTCACTCACTTGTCTTGGCGAGAAAGTATCCATCATGGTGTGATGCAATGCG 748
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 QY 749 GCGGCTGCATACGTTGATTCGGCTTACCTGCTTCCGACCAAGCGAATCATCGCAT 808
 Db 374 GCGGCTGCATACGTTGATTCGGCTTACCTGCTTCCGACCAAGCGAATCATCGCAT 433
 QY 809 CGACGAGCAGTACTCGGATGGAAGCGGCTTCTTGTGATCAGGATGATCTGGAGCAAGA 868
 Db 434 CGACGAGCAGTACTCGGATGGAAGCGGCTTCTTGTGATCAGGATGATCTGGAGCAAGA 493
 QY 869 GCATCAGGGGCTCGGCGCAGCGAATCTTTCGCCAGGCTCAAGCGCGCATGCCGACGG 928
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QY 1049 AGCGTTGGCTACCGTGATATTCTGAAGAGCTTGGCGGGAATGGCTGACCGCTTCCT 1108
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QY 1109 CGTGCTTTACGGTATCGCCGCTCCCGATTCGCGAGCGCATCGCCTTCTATCGCCTTCTTGA 1168
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Db 794 CGAGTTCTTCTGAG 807

RESULT 4
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DEFINITION EST750652 Nicotiana benthamiana mixed tissue cDNA library,
normalized, full-length Nicotiana benthamiana cDNA clone NEMBC75 5',
end, mRNA sequence.
ACCESSION CK287930
VERSION CK287930.1 GI:39864940
KEYWORDS EST.
SOURCE Nicotiana benthamiana
ORGANISM Nicotiana benthamiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
Staskawicz, B., Jin, H. and Baker, B.
Generation of EST sequences from Nicotiana benthamiana
Other ESTs: EST750653
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: ATT TAG GTG ACA CTA TAG.
Location/Qualifiers
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/organism="Nicotiana benthamiana"
/mol_type="mRNA"
/db_xref="taxon:4100"
/clone="NEMBC75"
/tissue_type="abiotic and biotic stress-treated leaves,
callus tissue and root tissue"
/lab_host="DH10B-Tona"
/clone_lib="Nicotiana benthamiana mixed tissue cDNA
library, normalized, full-length"
/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: RNA was isolated from Nicotiana benthamiana
tissues that include callus, roots from liquid culture
grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
challenged leaves (Pseudomonas syringae pv tomato 12 hr;
Xanthomonas campestris pv campestris 12 hr, 18hr;
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
amounts."

ORIGIN
Query Match 9.9%; Score 794; DB 14; Length 910;
Best Local Similarity 100.0%; Pred. No. 9.9e-108;
Matches 794; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 389 GATTGACAAAGATGATTGACGAGGTTCTCCGCGCGCTTGGGTGGAGAGGCTATTCCG 448
Db 4 GATTGACAAAGATGATTGACGAGGTTCTCCGCGCGCTTGGGTGGAGAGGCTATTCCG 63
QY 449 CTATGACTGGGCACAAACAGACAAATCGGTCTCTGTATGCGCGCGTGTTCGGCTGTACG 508
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Db 124 GCAGGGCGCGCGGTTCTTTTCTCAAGACCGACCTGTTCGGGTGCGCTGAATGAATGCA 183
QY 569 GGAACAGGAGCGCGGCTATCGTGGTGGCCACGAGCGGGCGTTCTTTCGCGAGCTGTGCT 628
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QY 629 CGAGCTTGTCTACTGAAGCGGGAAGGAGTGGTCTTATTTGGGCGAAGTGGCGGGGAGGA 688
Db 244 CGAGCTTGTCTACTGAAGCGGGAAGGAGTGGTCTTATTTGGGCGAAGTGGCGGGGAGGA 303
QY 689 TCTCCTGTCTATCTCACCTTCTCTCGCGAGAAAGTATCATCATGTGCTGATGCAATGCG 748
Db 304 TCTCCTGTCTATCTCACCTTCTCTCGCGAGAAAGTATCATCATGTGCTGATGCAATGCG 363
QY 749 CGCGCTGCATACGCTTGTATCCGGCTACTCCCATTCGACCCACCAAGCGAAACATCGCAT 808
Db 364 CGCGCTGCATACGCTTGTATCCGGCTACTCCCATTCGACCCACCAAGCGAAACATCGCAT 423
QY 809 CGAGCGAGCAGCTACTCGGATGGAAGCCGGTCTTTCGATCAGGATCATCTGGACGAGA 868
Db 424 CGAGCGAGCAGCTACTCGGATGGAAGCCGGTCTTTCGATCAGGATCATCTGGACGAGA 483
QY 869 GCATCAGGGCTCGCGCAGCGCAACTGTTCCGAGGCTCAAGGCGGCGCATGCCCGGCGG 928
Db 484 GCATCAGGGCTCGCGCAGCGCAACTGTTCCGAGGCTCAAGGCGGCGCATGCCCGGCGG 543
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Db 604 CCGCTTTTCTGGATTTCATCGACTGTGCGCGGCTGGGTGTGCGGACCGCTATCAGGACAT 663
QY 1049 AGCGTTGGCTACCGTGATATTCTGAAGAGCTTGGCGGCGGAATGGGCTGACCGCTTCCT 1108
Db 664 AGCGTTGGCTACCGTGATATTCTGAAGAGCTTGGCGGCGGAATGGGCTGACCGCTTCCT 723
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Db 784 CGAGTTCTTCTGAG 797

RESULT 5
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DEFINITION EST754513 Nicotiana benthamiana mixed tissue cDNA library,
normalized, full-length Nicotiana benthamiana cDNA clone NEMC477 5',
end, mRNA sequence.
ACCESSION CK291799
VERSION CK291799.1 GI:39872608
KEYWORDS EST.
SOURCE Nicotiana benthamiana
ORGANISM Nicotiana benthamiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
Staskawicz, B., Jin, H. and Baker, B.
Generation of EST sequences from Nicotiana benthamiana
Other ESTs: EST754514
Contact: Robin Buell
The Institute for Genomic Research
```

9712 Medical Center Dr, Rockville, MD 20850, USA
 Email: potato-array@tigr.org
 Clones can be requested from TIGR via potato@tigr.org
 Seq primer: ATT TAG GTG ACA CTA TAG.

FEATURES

source
 1..933
 /organism="Nicotiana benthamiana"
 /mol_type="mRNA"
 /db_xref="taxon:4100"
 /clone="NBMC477"
 /tissue_type="abiotic and biotic stress-treated leaves,
 callus tissue and root tissue"
 /lab_host="DH10B-Tona"
 /clone_lib="Nicotiana benthamiana mixed tissue cDNA
 library, normalized, full-length"
 /note="vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
 tissues: RNA was isolated from Nicotiana benthamiana
 grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
 cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
 challenged leaves (Pseudomonas syringae pv tomato 12 hr;
 Xanthomonas campestris pv campestris 12 hr, 18hr;
 Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
 campestris pv vesicatoria 18hr). RNA was isolated from
 these tissues and pooled in approximately equal molar
 amounts."

ORIGIN

Query Match 9.9%; Score 794; DB 14; Length 933;
 Best Local Similarity 100.0%; Pred. No. 9.8e-108;
 Matches 794; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 389 GATTGAACAGATGGATTGACGAGGTTCTCCGGCGCTTGGTGAGAGGCTATTCCG 448
 Db 46 GATTGAACAGATGGATTGACGAGGTTCTCCGGCGCTTGGTGAGAGGCTATTCCG 105

QY 449 CTATGACTGGGCAACAGCAATCGGCTGCTCTGATCGCGCGCTGTCGGCTGTGAGC 508
 Db 106 CTATGACTGGGCAACAGCAATCGGCTGCTCTGATCGCGCGCTGTCGGCTGTGAGC 165

QY 509 GCAGGGGCGCGGTTCTTTTGTCTAAGACCGACCTGTGCGGTGCCCTGAATGAATGCA 568
 Db 166 GCAGGGGCGCGGTTCTTTTGTCTAAGACCGACCTGTGCGGTGCCCTGAATGAATGCA 225

QY 569 GCAGGAGGCGAGCGGCTATCGTGGTGGCCAGCGAGCGGCTTCTTGGCGAGCTGTGCT 628
 Db 226 GCAGGAGGCGAGCGGCTATCGTGGTGGCCAGCGAGCGGCTTCTTGGCGAGCTGTGCT 285

QY 629 GCAGGTGTCTAGAGCGGGAAGGAGCTGGTGTCTATTGGGGAAGTCCCGGGGAGGA 688
 Db 286 GCAGGTGTCTAGAGCGGGAAGGAGCTGGTGTCTATTGGGGAAGTCCCGGGGAGGA 345

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 Db 346 TCTCTGTCTATCTCACTTGTCTTCTCCGAGAAATATCCATCAGTGTGATGCAATGCG 405

QY 749 CGGGCTGATAGCTTGTATCCGGCTACCTGCCATTCGACCAACGAGCAATCGCAT 808
 Db 406 CGGGCTGATAGCTTGTATCCGGCTACCTGCCATTCGACCAACGAGCAATCGCAT 465

QY 809 CGAGGAGGACGTAATCGGATGGAAGCGGCTTGTGATCAGGATGATCTGGAAGAGA 868
 Db 466 CGAGGAGGACGTAATCGGATGGAAGCGGCTTGTGATCAGGATGATCTGGAAGAGA 525

QY 869 GCATCAGGGGCTCGGCGAGCGAATGTTCCGAGGCTCAAGGCGCGCATGCCGACGG 928
 Db 526 GCATCAGGGGCTCGGCGAGCGAATGTTCCGAGGCTCAAGGCGCGCATGCCGACGG 585

QY 929 CGAGGATCTCGTGTGACCCATGCGGATGCTGCTTGGGAATATCATGTTGGAAATCG 988
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QY 989 CGGCTTTCTGGAATTCAGACTGTGGCGGCTGGGTGTGGCGGACCGCTATCAGGACAT 1048

Db 646 CCGCTTTCTGGAATTCAGACTGTGGCGGCTGGGTGTGGCGGACCGCTATCAGGACAT 705
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 Db 706 AGCGTTGGCTACCGCTGATATTGCTGAAGAGCTTGGCGGCAATGGCTGACCGCTTCT 765
 QY 1109 CGTGCTTTACGGTATCCCGCTCCCGATTCGACGCGCATCGCTTCTATCGCCTTCTTGA 1168
 Db 766 CGTGCTTTACGGTATCCCGCTCCCGATTCGACGCGCATCGCTTCTATCGCCTTCTTGA 825
 QY 1169 CGAGTCTTCTTGAG 1182
 Db 826 CGAGTCTTCTTGAG 839

RESULT 6
 CK256977
 LOCUS
 DEFINITION
 ESR740614 potato callus cDNA library, normalized and full-length
 Solanum tuberosum cDNA clone POC170 5' end, mRNA sequence.
 CK256977
 VERSION
 CK256977.1 GI:39813957
 EST
 SOURCE
 Solanum tuberosum (potato)
 ORGANISM
 Solanum tuberosum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamids; Solanales; Solanales; Solanaceae; Solanum.
 REFERENCE
 1 (bases 1 to 936)
 Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.
 Generation of ESTs from potato callus tissue
 Unpublished (2003)
 CONTACT: Robin Buell
 The Institute for Genomic Research
 9712 Medical Center Dr, Rockville, MD 20850, USA
 Email: potato-array@tigr.org
 Clones can be requested from TIGR via potato@tigr.org
 Seq primer: ATT TAG GTG ACA CTA TAG.

FEATURES
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 /organism="Solanum tuberosum"
 /mol_type="mRNA"
 /cultivar="Kennebec"
 /db_xref="taxon:4113"
 /clone="POCD170"
 /tissue_type="callus"
 /lab_host="DH10B-Tona"
 /clone_lib="potato callus cDNA library, normalized and
 full-length"
 /note="vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
 supplier: RNA was isolated from Solanum tuberosum var.
 Kennebec callus tissue grown on solid media."

ORIGIN
 Query Match 9.9%; Score 794; DB 14; Length 936;
 Best Local Similarity 100.0%; Pred. No. 9.8e-108;
 Matches 794; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 389 GATTGAACAGATGGATTGACGAGGTTCTCCGGCGGCTTGGTGAGAGGCTATTCCG 448
 Db 14 GATTGAACAGATGGATTGACGAGGTTCTCCGGCGGCTTGGTGAGAGGCTATTCCG 73

QY 449 CTATGACTGGGCAACAGCAATCGGCTGCTCTGATCGCGCGCTTGGTGAGAGGCTATTCCG 508
 Db 74 CTATGACTGGGCAACAGCAATCGGCTGCTCTGATCGCGCGCTTGGTGAGAGGCTATTCCG 133

QY 509 GCAGGGGCGCGGTTCTTTTGTCTAAGACCGAATCGTCCGCTGCCCTGAATGAATGCA 568
 Db 134 GCAGGGGCGCGGTTCTTTTGTCTAAGACCGAATCGTCCGCTGCCCTGAATGAATGCA 193

QY 569 GCAGGAGGAGCGGCTATCGTGGTGGCCAGCGGCGCTTCTTGGCGAGCTGTGCT 628


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Db      737 CGTGGCTTTACGGTATCGCGCTCCGATTCGACGCGATCGCTTCTATCGCCTTCTTGA 796
QY      1169 CGAGTTCTTCTGAG 1182
Db      797 CGAGTTCTTCTGAG 810

RESULT 8
CK283361
LOCUS   EST746083 Nicotiana benthamiana mixed tissue cDNA library,
DEFINITION normalized, full-length Nicotiana benthamiana cDNA clone NBMAG50 5'
end, mRNA sequence.
ACCESSION CK283361
VERSION   CK283361.1 GI:39855898
KEYWORDS EST.
SOURCE   Nicotiana benthamiana
ORGANISM Nicotiana benthamiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
REFERENCE 1 (bases 1 to 954)
AUTHORS   Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A., Day,B.,
           Staskawicz,B., Jin,H. and Baker,B.
TITLE     Generation of EST sequences from Nicotiana benthamiana
JOURNAL   Unpublished (2003)
COMMENT   Other ESTs: EST746084
           Contact: Robin Buell
           The Institute for Genomic Research
           9712 Medical Center Dr, Rockville, MD 20850, USA
           Email: potato-array@tigr.org
           Clones can be requested from TIGR via potato@tigr.org
           Seq primer: ATT TAG CTG ACA CTA TAG.
FEATURES   Location/Qualifiers
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                callus tissue and root tissue"
                /lab_host="DH10B-Tona"
                /clone_lib="Nicotiana benthamiana mixed tissue cDNA
                library, normalized, full-length"
                /note="Vector: pCMVSPORT6.1; Site.1: EcoRI; Site.2: NotI;
                supplier: RNA was isolated from Nicotiana benthamiana
                tissues that include callus, roots from liquid culture
                grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
                cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
                challenged leaves (Pseudomonas syringae pv tomato 12 hr;
                Xanthomonas campestris pv campestris 12 hr, 18hr;
                Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
                campestris pv vesicatoria 18hr). RNA was isolated from
                these tissues and pooled in approximately equal molar
                amounts."
ORIGIN
Query Match          9.9%; Score 794; DB 14; Length 954;
Best Local Similarity 100.0%; Pred. No. 9.7e-108;
Matches 794; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      389 GATTGAACAAGATGATTGCACGAGGTTCTCCGCCGCTTGGGGAGAGGCTATTCCG 448
Db      14  GATTGAACAAGATGATTGCACGAGGTTCTCCGCCGCTTGGGGAGAGGCTATTCCG 73
QY      449 CTATGACTGGGCACACAGACAATCGGTCTCTGATGCCGCCGTGTTCGGCTGTGAGC 508
Db      74  CTATGACTGGGCACACAGACAATCGGTCTCTGATGCCGCCGTGTTCGGCTGTGAGC 133
QY      509 GCAGGGGCGCCGGTCTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGCA 568
Db      134 GCAGGGGCGCCGGTCTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGCA 193

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QY      569 GGACGAGGAGCGCGGCTATCGTGGCTGGCCACGACGGCGTTCCTTTGCGCAGCTGTGCT 628
Db      194 GGACGAGGAGCGCGGCTATCGTGGCTGGCCACGACGGCGTTCCTTTGCGCAGCTGTGCT 253
QY      629 CGACGTTGTCACTGAAGCGGAGGAGGACTGGCTCTATTGGGGCGAAGTGCCTGGGGGAGGA 688
Db      254 CGACGTTGTCACTGAAGCGGAGGAGGACTGGCTCTATTGGGGCGAAGTGCCTGGGGGAGGA 313
QY      689 TCTCTGTCTATCTCACCTCTCTCCGAGAAAGTATCCATCATGCTGCTCATGCAATGCG 748
Db      314 TCTCTGTCTATCTCACCTCTCTCCGAGAAAGTATCCATCATGCTGCTCATGCAATGCG 373
QY      749 GCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCAACGCGAAACATCGCAT 808
Db      374 GCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCAACGCGAAACATCGCAT 433
QY      809 CGAGCGGAGCAGCTACTCGGATGGAAGCCGCTTTGTCGATCAGGATGATCTGACGAAGA 868
Db      434 CGAGCGGAGCAGCTACTCGGATGGAAGCCGCTTTGTCGATCAGGATGATCTGACGAAGA 493
QY      869 GCATCAGGGGCTCGCGCCAGCCGAACTGTTGCGCAGGCTCAAGGCGCGCATGCCGACGG 928
Db      494 GCATCAGGGGCTCGCGCCAGCCGAACTGTTGCGCAGGCTCAAGGCGCGCATGCCGACGG 553
QY      929 CGAGGATCTCTGCTGATGCCCATGGCGATGCTGCTTTCGCGAATATCATGCTGGAATG 988
Db      554 CGAGGATCTCTGCTGATGCCCATGGCGATGCTGCTTTCGCGAATATCATGCTGGAATG 613
QY      989 CGCTTTTCTGGATTCATGACTGTCGCGGCTGGGTGTGGCGGACCGCTATCAGGACAT 1048
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QY      1049 AGCGTTGGCTACCCGCTGATATTGCTGAAGAGCTTGGCGCGAATGGCTGACCGCTTCT 1108
Db      674 AGCGTTGGCTACCCGCTGATATTGCTGAAGAGCTTGGCGCGAATGGCTGACCGCTTCT 733
QY      1109 CGTGTCTTACGGTATCGCGCTCCCGATTCGAGGATTCGAGCGCATCGCTTCTATCGCTTCTGA 1168
Db      734 CGTGTCTTACGGTATCGCGCTCCCGATTCGAGGATTCGAGCGCATCGCTTCTATCGCTTCTGA 793
QY      1169 CGAGTTCTTCTGAG 1182
Db      794 CGAGTTCTTCTGAG 807

CK288185      811 bp mRNA linear EST 15-DEC-2003
EST750907 Nicotiana benthamiana mixed tissue cDNA library,
normalized, full-length Nicotiana benthamiana cDNA clone NBMBE61 5'
end, mRNA sequence.
CK288185
EST       CK288185.1 GI:39865462
SOURCE    Nicotiana benthamiana
ORGANISM  Nicotiana benthamiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
REFERENCE 1 (bases 1 to 811)
AUTHORS   Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A., Day,B.,
           Staskawicz,B., Jin,H. and Baker,B.
TITLE     Generation of EST sequences from Nicotiana benthamiana
JOURNAL   Unpublished (2003)
COMMENT   Contact: Robin Buell
           The Institute for Genomic Research
           9712 Medical Center Dr, Rockville, MD 20850, USA
           Email: potato-array@tigr.org
           Clones can be requested from TIGR via potato@tigr.org
           Seq primer: ATT TAG CTG ACA CTA TAG.
FEATURES   Location/Qualifiers
            source
              1..811

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/organism="Nicotiana benthamiana"
/mol_type="mRNA"
/db_xref="taxon:4100"
/clone="NMBB561"
/tissue_type="abiotic and biotic stress-treated leaves,
callus tissue and root tissue"
/lab_host="DH10B-Tona"
/clone_lib="Nicotiana benthamiana mixed tissue cDNA
library, normalized, full-length"
/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: RNA was isolated from Nicotiana benthamiana
tissues that include callus, roots from liquid culture
grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
challenged leaves (Pseudomonas syringae pv tomato 12 hr;
Xanthomonas campestris pv campestris 12 hr, 18hr;
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
amounts."

Query Match 9.7%; Score 778.8; DB 14; Length 811;
Best Local Similarity 99.7%; Pred. No. 1.8e-105;
Matches 780; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 386 CATGATTGAACAAGATGATGACGAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATT 445
Db |||||
30 CATGATTGAACAAGATGATGACGAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATT 89
Qy 446 CGGTATGACTGGGACACAGACAAATCGGTCTCTGATCCGCGCGTGTCCGGCTGTC 505
Db |||||
90 CGGTATGACTGGGACACAGACAAATCGGTCTCTGATCCGCGCGTGTCCGGCTGTC 149
Qy 506 AGCGAGGGGCGCGGTTCTTTTGTCAAGACCGACCTGTCCGGTGGCCCTGAATGAAT 565
Db |||||
150 AGCGAGGGGCGCGGTTCTTTTGTCAAGACCGACCTGTCCGGTGGCCCTGAATGAAT 209
Qy 566 GCAGGACGAGGACGCGGCTATCGTGGTGGCAGCGGCGTTCCTTGGCAGCTGT 625
Db |||||
210 GCAGGACGAGGACGCGGCTATCGTGGTGGCAGCGGCGTTCCTTGGCAGCTGT 269
Qy 626 GCTGACCTGTCACTGAAGCGGAGGAGTGGCTGTATTGGCGGAAGTGC CGGGGCA 685
Db |||||
270 GCTGACCTGTCACTGAAGCGGAGGAGTGGCTGTATTGGCGGAAGTGC CGGGGCA 329
Qy 686 GATCTCTGTCTCATCTCCTTCTCTCCGAGAAAGTATCCATCATGGCTGATGCAAT 745
Db |||||
330 GATCTCTGTCTCATCTCCTTCTCTCCGAGAAAGTATCCATCATGGCTGATGCAAT 389
Qy 746 GCGGCGGTGATAGCTTGTATCCGGCTACCTGCCCTTCCGACCAAGCGAAACATCG 805
Db |||||
390 GCGGCGGTGATAGCTTGTATCCGGCTACCTGCCCTTCCGACCAAGCGAAACATCG 449
Qy 806 CATGAGCGAGCAGCTACTCGATGGAAGCGGCTTGTTCGATCAGGATGATCTGAGCA 865
Db |||||
450 CATGAGCGAGCAGCTACTCGATGGAAGCGGCTTGTTCGATCAGGATGATCTGAGCA 509
Qy 866 AGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCCAGGCTCAAGGCGCGCATCCCGA 925
Db |||||
510 AGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCCAGGCTCAAGGCGCGCATCCCGA 569
Qy 926 GCGGAGGATCTGCTGATCCCATGCGATCGCTTGTCCGAAATATCATGCTGGAATA 985
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570 GCGGAGGATCTGCTGATCCCATGCGATCGCTTGTCCGAAATATCATGCTGGAATA 629
Qy 986 TGGCGCTTTTCTGGATTCATCGACTGTGCGCGCTGGGTGTGGCGGACCGGTATCAGGA 1045
Db |||||
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Qy 1106 CCTCGTGTCTTACGGTATCGCCGCTCCCGATTCGAGCGCATCGCTTCTATCGCCTTCT 1165
Db |||||
750 CCTCGTGTCTTACGGTATCGCCGCTCCCGATTCGAGCGCATCGCTTCTATCGCCTTCT 809
Qy 1166 TG 1167
Db ||
810 TG 811

RESULT 10
CK288711
LOCUS
DEFINITION
EST751433 Nicotiana benthamiana mixed tissue cDNA library,
normalised, full-length Nicotiana benthamiana cDNA clone NMBB149 5',
end, mRNA sequence.
CK288711 878 bp mRNA linear EST 15-DEC-2003
CK288711.1 GI:39866496
EST.
KEYWORDS
SOURCE
ORGANISM
Nicotiana benthamiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Nicotiana.
REFERENCE
AUTHORS
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
Staskawicz, B., Jin, H. and Baker, B.
TITLE
JOURNAL
COMMENT
Generation of EST sequences from Nicotiana benthamiana
Unpublished (2003)
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: ATT TAG GTG ACA CTA TAG.

FEATURES
source
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/organism="Nicotiana benthamiana"
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/db_xref="taxon:4100"
/clone="NMBB149"
/tissue_type="abiotic and biotic stress-treated leaves,
callus tissue and root tissue"
/lab_host="DH10B-Tona"
/clone_lib="Nicotiana benthamiana mixed tissue cDNA
library, normalized, full-length"
/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: RNA was isolated from Nicotiana benthamiana
tissues that include callus, roots from liquid culture
grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
challenged leaves (Pseudomonas syringae pv tomato 12 hr;
Xanthomonas campestris pv campestris 12 hr, 18hr;
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
amounts."

ORIGIN
Query Match 7.3%; Score 587; DB 14; Length 878;
Best Local Similarity 100.0%; Pred. No. 4.2e-77;
Matches 587; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 596 GSCACGACGGCGTTCCTTGGCAGCTGTCTCGACGTTGTCACTGAAGCGGGAAGGA 655
Db |||||
1 GSCACGACGGCGTTCCTTGGCAGCTGTCTCGACGTTGTCACTGAAGCGGGAAGGA 60
Qy 656 CTGGCTGTCTATTGGCGAAGTCCCGGGCAGATCTCTGTGATCTCACCTTGTCTCTGC 715
Db |||||
61 CTGGCTGTCTATTGGCGAAGTCCCGGGCAGATCTCTGTGATCTCACCTTGTCTCTGC 120
Qy 716 CGAAGAAATTCATCGCTGATGCGGCTGATGCGGCTGATGCTGATGCTGCTGCTAC 775
Db |||||

121 CGAGAAAGTATCCATCATGGCTGATCAATGCGCGCTGCATACGCTTTGATCCGGCTAC 180
QY 776 CTGCCATTGACCCACAGCGAAACATCGATCGAGCGAGACGCTACTCGATGGAAC 835
Db 181 CTGCCATTGACCCACAGCGAAACATCGATCGAGCGAGACGCTACTCGATGGAAC 240
QY 836 CGGTCTTGTGATCAGATGATCTGACGAAGAGCATCAGGGGCTCGCGCCAGCCAACT 895
Db 241 CGGTCTTGTGATCAGATGATCTGACGAAGAGCATCAGGGGCTCGCGCCAGCCAACT 300
QY 896 GTTCGCGAGCTCAAGCGCGGATGCGCGAGCGAGATCTGCTGATGCCAATGGCGA 955
Db 301 GTTCGCGAGCTCAAGCGCGGATGCGCGAGCGAGATCTGCTGATGCCAATGGCGA 360
QY 956 TGCTGCTTGGCGGAATATCATGTTGAAATGCGCGCTTTCTGATTCATGACATGTTG 1015
Db 361 TGCTGCTTGGCGGAATATCATGTTGAAATGCGCGCTTTCTGATTCATGACATGTTG 420
QY 1016 CGGGTGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGTACCGGTGATATTGCTGA 1075
Db 421 CGGGTGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGTACCGGTGATATTGCTGA 480
QY 1076 AGAGCTTGGCGGGAATGGGCTGACCGCTTCCTGCTGCTTTACGATACCGCGCTCCCGA 1135
Db 481 AGAGCTTGGCGGGAATGGGCTGACCGCTTCCTGCTGCTTTACGATACCGCGCTCCCGA 540
QY 1136 TTTCGAGCGCATCGCTCTCTATCGCTTCTTACGAGTCTTCTGAG 1182
Db 541 TTTCGAGCGCATCGCTCTCTATCGCTTCTTACGAGTCTTCTGAG 587

RESULT 11
A0361914
LOCUS
DEFINITION
mgxb0005K01f CUGI Rice Blast BAC Library Magnaporthe grisea genomic
clone mgxb0005K01f, genomic survey sequence.

ACCESSION
VERSION
A0361914.1 GI:4211753
KEYWORDS
GSS.
SOURCE
Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.
1 (bases 1 to 789)
AUTHORS
Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
Phillips, K., Sasinsowski, M., Wing, R.A. and Dean, R.A.
TITLE
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
Genome

Unpublished (1998)
CONTACT: Dean RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson University, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemson.edu

Seq primer: TAATACGATCTACTATAGGG
Class: BAC ends
High quality sequence start: 41
High quality sequence stop: 392.
Location/Qualifiers

1..789
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/clone="mgxb0005K01f"
/tissue_type="Protoplasts"
/lab_host="E. coli DH10B"
/clone_lib="CUGI Rice Blast BAC Library"
/note="Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII;
Rice blast is one of the most devastating fungal diseases
of rice world wide. It is a filamentous ascomycete with

FEATURES
source

RESULT 12
A0398387

LOCUS
DEFINITION

mgxb0009J05f CUGI Rice Blast BAC Library Magnaporthe grisea genomic
clone mgxb0009J05f, genomic survey sequence.

ACCESSION
VERSION
A0398387.1 GI:4369414

KEYWORDS
GSS.
SOURCE
Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.
1 (bases 1 to 620)

REFERENCE
AUTHORS
Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
Phillips, K., Sasinsowski, M., Wing, R.A. and Dean, R.A.

TITLE
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
Genome

Unpublished (1998)

a haploid genome (n=7) of approximately 40 Mbp. Rice
blast is an important model fungal pathogen for studying
numerous aspects of the fungal-host interaction. In
order to facilitate genome wide analysis, a BAC library
containing 9216 clones with an average insert size of 130
kbp was constructed. This library represents greater
than 25X genome coverage. High density colony filters
are available upon request."

ORIGIN

Query Match 7.2%; Score 577.4; DB 28; Length 789;
Best Local Similarity 97.8%; Pred. No. 1.1e-75;
Matches 584; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 581 GGGCTATCTGTGGTGGCCACGACGGGCGTTCTTGGCGAGCTGTCTCGAGCTTGTCTAC 640
Db 39 GNGGCTATCTGTGGTGGCCACGACGGGCGTTCTTGGCGAGCTGTCTCGAGCTTGTCTAC 98

QY 641 TGAAGCGGGAAGGAGTGGCTGCTATTGGGCGAAGTGGCGGGCAGGATCTCTGTCTATC 700
Db 99 TGAAGCGGGAAGGAGTGGCTGCTATTGGGCGAAGTGGCGGGCAGGATCTCTGTCTATC 158

QY 701 TCACCTTGTCTTGGCGGAGAAAGTATCCATCATGTGCTGATGCAATGCGCGGCTGCATAC 760
Db 159 TCACCTTGTCTTGGCGGAGAAAGTATCCATCATGTGCTGATGCAATGCGCGGCTGCATAC 218

QY 761 GTTGTATCGGCTACTGTGCCATTTCGACCAAGGAAATCGCATCGAGCGAGCAGC 820
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mgxb0009J05f CUGI Rice Blast BAC Library Magnaporthe grisea genomic
clone mgxb0009J05f, genomic survey sequence.

AQ398387
GSS.
Magnaporthe grisea (anamorph: Pyricularia grisea)

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.
1 (bases 1 to 620)

REFERENCE
AUTHORS
Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
Phillips, K., Sasinsowski, M., Wing, R.A. and Dean, R.A.

TITLE
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
Genome

Unpublished (1998)

```

COMMENT      Contact: Dean RA
              Clemson University
              100 Jordan Hall, Clemson University, Clemson, SC 29634
              Tel: 864 656 5737
              Fax: 864 656 4293
              Email: rdean@clemson.edu
              Seq primer: TAATACGACTCACTATAGGG
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Rice blast is one of the most devastating fungal diseases
of rice world wide. It is a filamentous ascomycete with
a haploid genome (n=7) of approximately 40 Mbp. Rice
blast is an important model fungal pathogen for studying
numerous aspects of the fungal-host interaction. In
order to facilitate genome wide analysis, a BAC library
containing 9216 clones with an average insert size of 130
kbp was constructed. This library represents greater
than 25X genome coverage. High density colony filters
are available upon request."

FEATURES             source
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kbp was constructed. This library represents greater
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ORIGIN
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Matches 564; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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QY 669 GGCGAAGTGGCGGGCAGGATCTCTGTCACTCACTTGTCTCTGCGGAGAAAGTATCC 728
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QY 729 ATCATGGCTGATCAATGCGGCGGTGCATACGCTTGATCGGCTACTCGGCCATTGAC 788
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DEFINITION 561 bp DNA linear GSS 08-APR-1999
clone mgxb0012I01f CUGI Rice Blast BAC Library Magnaporthe grisea genomic
clone mgxb0012I01f, genomic survey sequence.
ACCESSION AQ447874
VERSION   AQ447874.1 GI:45777011
KEYWORDS  GSS.
SOURCE    Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM  Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.
1 (bases 1 to 561)
Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
Phillips, K., Sasincowski, M., Wing, R.A. and Dean, R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
Genome
Unpublished (1998)
Contact: Dean RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson University, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemson.edu
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Rice blast is one of the most devastating fungal diseases
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kbp was constructed. This library represents greater
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are available upon request."

ORIGIN
Query Match      6.4%; Score 514.8; DB 28; Length 561;
Best Local Similarity 99.6%; Pred. No. 2.2e-66;
Matches 516; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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clone mgxb0011E13f, genomic survey sequence.
ACCESSION AQ447775
VERSION 1
SOURCE GSS.
ORGANISM Magnaporthe grisea (anamorph: Pyricularia grisea)
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.
Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.
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Genome
Unpublished (1998)
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Clemson University Genomics Institute
100 Jordan Hall, Clemson University, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemson.edu
Seq primer: TAATACGACTCACTATAGG
Class: BAC ends
High quality sequence stop: 342.
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kbp was constructed. This library represents greater
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are available upon request."

Query Match 6.4%; Score 508; DB 28; Length 509;
Best Local Similarity 100.0%; Pred. No. 2.3e-65;
Matches 508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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clone mgxb0006O09f, genomic survey sequence.
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VERSION 1
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SOURCE GSS.
ORGANISM Magnaporthe grisea (anamorph: Pyricularia grisea)
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.

REFERENCE 1 (bases 1 to 637)
AUTHORS Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.
TITLE A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
Genome
JOURNAL Unpublished (1998)
COMMENT Contact: Dean RA
Clemson University Genomics Institute
100 Jordan Hall, Clemson University, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemson.edu
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ORIGIN

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Qy 1156 ATCGGCTTCTTGACGAGTTCTTCTGAG 1182
Db 481 ATCGGCTTCTTGACGAGTTCTTCTGAG 507

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